(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
26 July 2001 (26.07.2001)

PCT

(10) International Publication Number
WO 01/53312 A1

WO 01/53312 A1

(51) International Patent Classification[7]: C07H 21/04, C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00

(21) International Application Number: PCT/US00/34263

(22) International Filing Date:
26 December 2000 (26.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US
09/598,042	9 July 2000 (09.07.2000)	US
09/620,312	19 July 2000 (19.07.2000)	US
09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/488,725 (CIP)
Filed on	21 January 2000 (21.01.2000)
US	09/552,317 (CIP)
Filed on	25 April 2000 (25.04.2000)
US	09/598,042 (CIP)
Filed on	9 July 2000 (09.07.2000)
US	09/620,312 (CIP)
Filed on	19 July 2000 (19.07.2000)
US	09/653,450 (CIP)
Filed on	3 August 2000 (03.08.2000)
US	09/662,191 (CIP)
Filed on	14 September 2000 (14.09.2000)
US	09/693,036 (CIP)
Filed on	19 October 2000 (19.10.2000)
US	09/727,344 (CIP)
Filed on	29 November 2000 (29.11.2000)

(71) Applicant *(for all designated States except US)*: **HYSEQ, INC.** [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **TANG, Y., Tom** [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). **LIU, Chenghua** [CN/US]; 1125 Ranchero Way #14, San Jose, CA 95117 (US). **ASUNDI, Vinod** [US/US]; 709 Foster City Boulevard, Foster City, CA 94404 (US). **CHEN, Rui-hong** [US/US]; 1031 Flying Fish Street, Foster City, CA 94404 (US). **MA, Yunqing** [CN/US]; 280 W. California Avenue #206, Sunnyvale, CA 94086 (US). **QIAN, Xiaohong, B.** [CN/US]; 3662 Tumble Way, San Jose, CA 95132 (US). **REN, Feiyan** [US/US]; 7703 Oak Meadow Court, Cupertino, CA 95014 (US). **WANG, Dunrui** [CN/US]; 932 La Palma, Milpitas, CA 95035 (US). **WANG, Jian-Rui** [CN/US]; 744 Stendhal Lane, Cupertino, CA 95014 (US). **WANG, Zhiwei** [CN/US]; 836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US). **WEHRMAN, Tom** [US/US]; 3210 CCSR Mol. Pharm, 269 W. Campus Drive, Stanford, CA 94305 (US). **XU, Chongjun** [CN/US]; 4918 Manitoba Drive, San Jose, CA 95130 (US). **XUE, Aidong, J.** [CN/US]; 1621 S. Mary Avenue, Sunnyvale, CA 94087 (US). **YANG, Yonghong** [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). **ZHANG, Jie** [CN/US]; 4930 Poplar Terrace, Campbell, CA 95008 (US). **ZHAO, Qing, A.** [CN/US]; 1556 Kooser Road, San Jose, CA 95118 (US). **ZHOU, Ping** [CN/US]; 1461 Japaul Lane, San Jose, CA 95132 (US). **GOODRICH, Ryle** [US/US]; 4896 Sandy Lane, San Jose, CA 95124 (US). **DRMANAC, Radoje, T.** [YU/US]; 850 East Greenwich Place, Palo Alto, CA 94303 (US).

(74) Agent: **ELRIFI, Ivor, R.**; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

WO 01/53312 A1

WO 01/53312 A1

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

BEST AVAILABLE COPY

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g., in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1+4^{25}$) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or cukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli,* will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 ; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358 ; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*,

hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following

vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for

transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO:1-1786 and 3573-5358 , antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the

inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA

portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, Proc. *Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359-7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1787-3572 and 5359-7144.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: *A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.
In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10; B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoictic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

(ii) increased sprouting of neurons in culture or in vivo;

(iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or

(iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01μg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1μg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with

an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions

may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which

modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the

population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50}. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.
The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.
The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse™ as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular

defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and

software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm$_7$), is then added to a final concentration of 10 mM 1-MeIm$_7$. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm$_7$, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (*no* preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm^2, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1.1 EXAMPLE 1

<u>Novel Nucleic Acid Sequences Obtained From Various Libraries</u>

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.1.2 EXAMPLE 2

Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

5.2.2 EXAMPLE 3

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genebank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1- 327.

Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept . The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.3.2 EXAMPLE 4

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the cMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.3.2 EXAMPLE 5

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.4.2 EXAMPLE 6

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.5.2 EXAMPLE 7

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119, UniGene version 119, Genpept release 119). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0nl 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.6.2 EXAMPLE 8

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	9 19-21 50-51 65-66 72 78 80 82 85 87 107-108 113 116 123 138 140 150-152 159 169 177 192-193 202-203 212-214 225-226 235-236 251 258 268-269 272 280-281 295 298 301 321 326 331-332 334 356-357 362 369 379 382-383 416 423 443 459-460 473 475 477 488 496 500 503 519 526 547 574 582 587 608-609 613 618 633-634 645-646 652 657-658 660 669-671 678 687 695 697 710 715 724 731 775-777 796 804 811 857-859 862 869 899-900 912 919 922 924-929 933 936 962 979 988-989 996 1001 1004-1008 1018 1039 1047 1059 1064 1067 1070 1078 1082 1107 1113 1116-1117 1131 1134-1137 1140 1149 1151 1157 1180 1206 1229 1234 1241 1243 1258 1272-1273 1279 1288-1290 1294 1307-1308 1312 1320 1323 1330 1356 1360-1361 1368 1373-1375 1379 1391 1400 1417 1446 1468 1482 1493-1494 1501-1503 1506-1507 1512 1517 1522-1524 1530-1533 1537 1549 1565 1578 1598 1606 1608 1623 1625 1627 1639 1643 1648-1649 1653 1664 1667 1671 1696 1734 1741 1743-1744 1760-1761 1771
adult brain	GIBCO	ABD003	3 12-14 18-19 25 30-31 34-36 43-45 50-51 56 58 60 65-66 68-69 80 82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192-193 196-197 199 203 208 210 212-214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284-288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476-478 483 491 494 496 500 503 507-508 516 519-520 525-527 534 536-540 542-543 545 553 555 560 569-570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993 997-1001 1005-1007 1012 1017-1020 1023-1024 1029-1031 1034 1036 1039 1050 1059 1063-1066 1078 1081-1082 1085-1086 1089

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1097 1103 1107 1109 1112 1116-1117 1119 1121 1124 1127 1130 1134 1144-1145 1149 1151 1157-1158 1167 1170 1178 1184 1188 1190 1193-1194 1200 1202 1215-1217 1220 1226-1227 1229 1231 1241 1243 1247 1252 1258 1263 1267 1269 1279 1281 1284 1286-1289 1293-1294 1306-1307 1312 1316-1320 1326 1333 1338 1341 1344 1348 1351 1355-1357 1360 1374 1377 1380 1386 1389-1390 1394 1400 1409 1414 1422-1423 1425-1427 1437 1443 1446 1454 1456 1458-1459 1468 1470-1472 1478 1482-1483 1487-1488 1493 1497 1499 1506 1508-1511 1517 1522-1524 1530-1533 1545-1546 1548-1550 1552 1557-1559 1563 1565 1567 1569 1571 1586 1588 1591 1593 1595 1598-1601 1608 1611 1620-1621 1624-1626 1628 1630-1632 1636 1640-1641 1644-1645 1647 1649 1653-1655 1657 1664 1667 1669 1673 1678-1681 1686 1690 1694-1696 1701 1709 1711 1719 1722-1723 1726-1727 1731-1733 1738 1740 1743-1744 1747 1749 1753 1757-1758 1760-1761 1765 1771 1785
adult brain	Clontech	ABR001	9 29 68-69 113 115 146 152 206 223 245 277 307 320 324 330-331 344 348 352 362 379 384 393 404 408 414 441-442 454 469 481 490 506 517 586 597 631 641 659 691 715 799 803 833 865 871 875 880 882 908 920 937 1000 1005-1006 1027 1036 1041 1043 1075 1107 1112 1121 1127 1136-1137 1144-1147 1231 1238-1239 1280 1293 1320 1345 1355 1361 1383-1384 1400 1417 1448 1456 1476 1507 1570 1572 1609-1610 1614 1620 1626 1645 1653 1754 1759 1770 1786
adult brain	Clontech	ABR006	5-8 15-16 168 212-213 271 278 280-281 291-292 300-301 310 314 321 326 336-338 341 352 357 359-360 362 369 374 379 384 393 396-397 414 419-420 426-428 430 441-442 453 506 616-617 661 689 785 798 845 1018 1109 1113 1124 1148 1167 1187 1207 1227 1262 1265 1285 1312 1317-1319 1324-1327 1344 1369 1381 1400 1416 1421 1427 1430-1431 1436 1471 1501 1557-1559 1586 1588 1651 1653 1664-1665 1671 1673 1690 1697-1698 1700 1711 1717 1719-1720 1728 1736 1740 1743-1744 1757 1760-1761
adult brain	Clontech	ABR008	5-10 13-19 22-23 25 29 33 37-39 43-45 50-51 54-55 57-58 60-66 68-70 72 75 77-80 83 85 89-92 94 99-105 108-110 112-113 116-117 123 128 133 135-137 139 143 145-146 148 152 154-155 157 166 168-172 174-175 181-184 188-190 193-194 196 198-200 202 204-205 207-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			208 210 214-215 218 221-226 229 231-232 234-241 245-247 251-253 255 257-259 268-269 271 276-281 285-286 288 290-292 300-302 304 307 309-311 313 315 317-318 320-322 325-326 328 330-331 333-338 341 344-347 349 352 354 356-357 362 369-373 376 379-380 382 384 387 390-391 393-394 397 399-403 405-411 414-415 417-420 426-428 437-438 440-444 453-455 462 464 467 469-471 476 478 482-484 488-491 497 503 506-513 516-517 520 524-526 528-530 532-534 537-540 542 544 547-551 553 561 565-567 572-574 577 581 585 587-588 590-591 597 599 601-602 606-610 612 615-617 619-620 622-623 628-629 631 633-634 636-641 643 645-647 651-653 655-664 669-671 673 679 682 687 689 691-700 702 706 710 715-717 720-721 725-734 736-739 742-743 746 750-752 756 758-759 762-764 766 768 773-778 780-782 784-785 787-789 794 796 799 802-803 805 811 814-815 818 825-826 834-837 839-840 842-843 856-859 861-862 865 867-872 874-875 881 883-884 887 889-892 894-895 897-898 901 904 908 910 912 914 917 919 921-924 926-927 930-932 935-941 943 945 949 953-954 958 961-963 967 969 971 975 977 981-983 986 988-990 992 997 999-1002 1004-1006 1008 1012 1018-1023 1027 1029-1031 1035-1037 1047-1048 1053 1057 1059 1063 1068 1070 1072-1075 1077 1081-1083 1085-1093 1095-1096 1108-1112 1114-1125 1127 1131-1133 1135-1138 1142-1145 1148-1158 1160-1163 1167 1169 1172 1175 1177 1180 1183-1188 1191-1195 1199-1200 1204 1206 1211 1213-1216 1222-1223 1226-1227 1229-1231 1234-1235 1241-1242 1244-1263 1266 1269-1271 1276-1277 1279-1281 1284-1286 1292 1294-1295 1299 1305-1309 1312 1314 1316-1319 1322 1324-1327 1330 1332 1334-1335 1339 1344-1346 1351 1354-1355 1357-1358 1365-1367 1369-1370 1373-1374 1376-1379 1381-1384 1386-1388 1392 1394 1396-1397 1400 1403-1407 1410 1414 1419-1420 1423 1432-1433 1435 1437-1438 1440-1442 1446 1448 1453-1455 1457 1461 1463-1464 1466 1468 1471 1477 1480 1482-1483 1496 1502-1504 1507-1509 1513 1519-1520 1524-1526 1536 1547 1549-1552 1567 1573-1574 1578 1586-1589 1597-1598 1601-1602 1605 1607-1609 1611-1617 1619-1621 1623 1625-1626 1635-1641 1643-1645 1649 1651 1653 1656-1658 1664 1669 1671-1674 1676-1684 1686 1689-1690 1694-1696 1704-1705 1708-1709

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1720-1724 1726-1728 1730-1733 1737-1740 1742-1745 1753 1756-1757 1759-1761 1765 1767 1771-1772 1776-1777 1779-1780 1786
adult brain	Clontech	ABR011	24 75 103 186 210 310-311 364-365 508 623 710 937 1002-1003 1059 1204 1609 1731-1732
adult brain	BioChain	ABR012	46 182-184 204-205 300 739 767 1371 1549 1620 1684
adult brain	Invitrogen	ABR013	185 204-205 364-365 393 497 595 687 692-694 830 845 1068 1320 1413 1640
adult brain	Invitrogen	ABR014	187 301 357 364-365 375 454 463 731 859 939 983 1073 1262 1270 1320 1403 1640 1651 1657 1696 1722 1738
adult brain	Invitrogen	ABR015	419 434-435 441-442 763 789 983 1320
adult brain	Invitrogen	ABR016	312 364-365 379 1320 1334-1335 1674 1722 1785
adult brain	Invitrogen	ABT004	14-16 22-23 25 37-39 43 58 60 70-72 78 86 94 107 113 116 136-137 143 146 152 161 173 182-184 194 196 198 210 218 229 259 267 295 298 309-310 320-321 324 336-338 346-347 349-350 356-357 362 371 379-380 382-383 391 393 396 399 401 408 428 438 459 461 476 482 490 502 507-509 516 526 531 557 562 597 602 607-609 624 652 655 667 669 671-672 687-689 695-696 710 712 715 721 732 739 743 750 753 766 778 780-781 789 803 814 826 830 837 841 857 869 874 894-895 925 937 949 954-956 960-961 963 968-969 988-989 1000 1005-1006 1016-1019 1021 1036-1037 1052 1086 1090 1109 1113 1115 1120-1121 1123-1124 1136-1137 1140 1144-1147 1151 1167 1170 1174 1188 1193-1194 1205 1225 1229 1231 1254 1258 1262 1280 1285 1309 1312 1334-1335 1341 1343-1344 1356-1357 1370 1378-1379 1383-1384 1403-1404 1423 1429 1434 1442 1448 1451-1452 1454 1470-1472 1482 1499 1525 1528-1529 1532 1536 1547 1554 1557-1559 1561-1562 1567 1585 1588 1590 1595 1601-1604 1608 1610-1613 1615 1619 1624 1627 1640 1644 1647 1660 1664 1666 1670 1675 1696 1704 1715 1723 1727 1738 1760-1761 1768 1779 1785-1786
cultured preadipocytes	Strategene	ADP001	5-8 11 17 25 68-69 80 82 87 103 105 110 116 136-138 168 171 188-189 196-198 261 267 276 288 293 301 318 331 336-338 379-380 391 400 428 430-431 510-512 520 524 527 549 557 561 602 618 620 622 631 637 647 670 681-682 710 731 748 782 793-794 817 834-836 843 845 858-859 879 882 893-895 934 960 982 986 995-996 1000 1002 1005-1007 1025 1027-1028 1032 1039 1045 1071 1078 1097 1099-1102 1136-1137 1140 1219-1220

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1260 1271 1297-1298 1314 1320 1322 1329 1339 1345 1365-1366 1370-1371 1398 1408 1423 1431 1437 1466 1468 1533 1539 1594 1602 1608 1614 1631 1649-1650 1660 1662 1673 1687-1688 1696 1711 1719-1720 1742 1746 1749 1760-1761 1765 1767 1771 1785
adrenal gland	Clontech	ADR002	4-10 15-16 25 29-31 43-45 47 50-51 55 60 62-63 65-66 75 80 102 116 118 122 126 130 137 150 169-170 181 192 198 201-203 215 227-228 247 251 255 267-269 271 280-281 285 295 298 311 336-338 342 349 351-352 354 372-373 383-385 391 400 410 415-416 424 426-427 431 434-437 439 445 454 461 473 477 483 491 493 497-498 503 516 519 527 535 546 549 552 572-573 581 588 595 600 602 608-610 620 628-630 637 645-646 670 679 703 713 715 719 732 734 744-746 758 773-778 789 816 829 837 845 848 869 875 883 898 904 912 922-923 930-931 942 948 952 965 967 969 976-977 981 990 992-993 1001 1004 1049 1055 1059 1071-1072 1076 1112-1113 1115 1121 1127 1134-1135 1151 1158 1163 1175 1181 1188 1209 1218 1224-1225 1227 1231 1243 1270-1271 1274 1280 1285 1290 1293 1307 1324-1325 1327 1330 1342-1343 1345 1348 1365-1366 1369 1378-1379 1387 1398 1400 1405 1417 1425-1426 1436 1440-1441 1444 1454 1463-1464 1488 1491 1507 1512 1538 1546 1567 1573-1575 1588 1598 1609 1614 1618 1622 1624 1627 1634 1636 1649 1651 1658 1671 1674 1678-1679 1691-1692 1703 1717 1727 1731-1732 1737 1765
adult heart	GIBCO	AHR001	4-8 10-11 15-16 18-21 34-39 44-46 50-52 57-58 60 62-63 71 75 82 85 87 89 94 97 100 103-104 108-110 112 114 116 118-119 122-123 127 130-132 134 136-138 141-144 147-151 153 163-164 168-171 179 186 192 195 197 199 204-205 212-215 220 225-226 229-230 232 234-236 251 257-260 262 265 272 274 277 280-282 285-286 289-292 296 298-301 304 307 309 314 321 324-325 330 333 336-338 345 349 351-352 354 358 361 368 370 380 383-384 387-388 391 393 397 401 406 408-409 411-412 414-416 430-431 433-439 445-446 449 452 454-455 457 459 462 469 472-473 476-480 483-484 487-490 492-493 496-498 503 506 508 510-513 516 519-522 526 534 536-540 542 546 549 553 560-562 574-577 581-582 584 586-587 589 593 595 597 604-609 611-612 615-620 622-623 626 632 637 645-652 656-660 665-666 670-672 674-675 683-684 687 692-694 697 701 709 712 715-716 719-720 725-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			726 728 730-732 735 738-739 743-744 746 751 753 759 761 765 770-771 775-780 785 788-790 796 802 804 810 812 817 821 826 828 830 837 843 845-847 849-853 857-861 863-864 869 871 875 877-879 881 883 887 890-892 894-895 897-898 901 903 906-907 911-913 915 919 921-925 927-928 933-935 945 950 961-963 967 969-972 975 977-978 980-986 990 992 999-1002 1005-1007 1010 1016 1019-1020 1022-1023 1025 1028-1037 1039-1040 1043 1047 1050 1054-1055 1057 1059 1063-1064 1067-1068 1070 1072 1075-1076 1083 1085-1087 1089 1093-1094 1104 1106 1108-1109 1113 1116-1117 1119 1121 1124 1126 1128 1131-1134 1144-1145 1148-1149 1151 1158 1167 1169-1170 1175 1177 1192 1196 1199-1200 1202 1206-1208 1211 1216 1218 1222 1227-1229 1232-1235 1238-1241 1243-1244 1247-1248 1250 1253-1254 1256-1258 1261 1268 1270-1271 1277 1280-1282 1287 1292 1298-1299 1306 1308 1317-1321 1324-1325 1330 1332 1334-1337 1339 1344-1345 1349-1350 1354-1356 1359-1360 1365-1366 1369 1371 1374-1375 1378-1380 1383-1384 1389 1397 1400 1403 1409 1417 1423-1426 1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536-1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644-1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743-1744 1749 1754-1755 1760-1761 1765 1772 1785
adult kidney	GIBCO	AKD001	4-8 10-11 17-21 29-31 35-39 42-45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102-104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215-216 223-228 234-236 238 247 251-253 257-259 261-262 265-269 271-272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331 333 341 344 348-350 352 356 358-359 362 364-365 368 370-372 374 376-377 380-382 392 395 398 400-401 404 407-409 414-415 423-424 430-437 443-444 446 449 451 453-455 459 461-462 464 467 469 471-474 476-477 480-481 483 487-488

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			490-491 493 497-505 510-513 516-520 522 524 526-529 534 537-540 544 547 549 554-556 560 562 564 567 571-576 578 582 586-589 592-593 598-599 601 604-606 608-613 615-619 621-626 632-634 637-643 645-652 655 660-664 669-672 676 678-679 688 692-695 698 702 711 713 717 719-720 727 731 735-736 738 743 745-746 751 753 755 762-763 765 771-773 775-778 780 786 788 793 795-796 800 803 805 808 810-812 814-819 821 826 829 832 834-838 842-845 848-855 857-861 864-865 867 869 871 874 876-883 886-887 889-891 893-896 898-900 902 906-908 910-914 918 920 922 925-927 929-935 937 940-942 945 948-949 951 953-958 960-961 963-964 969-970 972 976-978 982-986 988-990 992-993 995-997 999-1002 1004-1008 1010 1012-1013 1016-1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088-1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142-1143 1146-1147 1149-1150 1153-1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196-1200 1202-1204 1206-1211 1216-1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317-1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-1443 1445-1446 1448-1450 1453-1454 1459 1461 1465-1468 1474-1475 1478 1484-1488 1490 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540-1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603-1604 1606 1608 1611 1613 1615-1616 1618-1622 1624-1628 1631-1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676-1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785
adult kidney	Invitrogen	AKT002	20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133 136-137 140 142-143 149 169 174

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			181 197 227-228 235-236 244 251 261-265 267 280-281 286 290 299 301 304-305 309 312-313 339 341 344-345 349 358 370-372 376 382-383 387 392 401 414 416 421 430 443 445 449 453-454 472 487-488 504 506 513 516 519 522 528 536-540 546 554 585 587 594 598 602 607 616-617 626-627 636 643 662-664 695 709 721 735 743 761 768 775-777 788 796 804 814 827 837-838 849-850 852-853 869-870 881 890-892 898 903 905-907 914 919 925 927 934 941 949 952 957 960 962 968 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110-1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324-1325 1330 1344 1349 1351 1355-1356 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477-1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669-1670 1673 1686 1709 1727 1740 1776
adult lung	GIBCO	ALG001	4-8 14 37-39 44-46 50-51 56 62-63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553-1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786
lymph node	Clontech	ALN001	4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280-281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-482 503 526 529 537-540 546-547

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			621 626 649 679 719 725-726 738 793 803 831 834-836 838 844 857-858 866 879 905 913 928 963 976 1005-1006 1012 1038 1050 1116-1117 1151 1199 1204 1226 1243 1265 1274 1324-1325 1339 1353 1374 1377 1440-1442 1447 1504 1549 1600 1618-1619 1631 1641 1644 1653 1687-1688 1691-1692 1741 1771
young liver	GIBCO	ALV001	5-8 11 20-21 46 50-51 58 65-66 75 79 82 93 97 102-103 108 110 116 139 143-144 148-149 171-172 174 187-189 194-195 198 209 214-215 230 250 258 267-269 280-281 306 309 342 351 356 359 362 372 374 392 394 398 401 407-408 410 414 431 444 455 459 476 478 483 493 510-512 516 520 522 526 536 549 571 574-577 585 592 601-602 607 621-624 628-630 632-633 637 648 660 666-667 678 697-698 700 717 719 728 730 734 738 744-745 766 770 773 779 788 800 808 812 814 841 849-851 871 874 879 887 893 898-900 902-904 906-907 911 919 922 924 934 953 957 963 965 970 984 986 997 1001 1004 1007 1012 1029-1030 1033-1034 1052 1061 1066 1070 1076 1086 1089 1093 1099-1102 1110-1112 1116-1117 1119 1121 1125 1136-1137 1144-1145 1156-1157 1159 1196 1199-1200 1209 1211 1219-1220 1241 1244 1262 1270 1275 1279 1283 1295 1317-1320 1332 1339 1344 1359 1362-1363 1379 1383-1384 1403 1415 1430-1431 1437 1450 1467 1475-1476 1483-1484 1494-1495 1498 1505 1512 1516 1518-1519 1526 1529 1547 1550-1552 1557-1559 1565 1583 1587 1597 1609 1614 1620 1631 1637 1641 1644 1654-1655 1662 1667 1669 1684 1691-1692 1702 1711 1725 1738 1741 1743-1744 1758 1760-1761 1763-1765 1769
adult liver	Invitrogen	ALV002	5-8 17 20-21 32-33 41 55 58 64 75 77 86 89 102 108 117 119 175-176 198 200 209 231 235-236 250 272 275-276 284 306 316 321 325 333 356 359 374 376 398 401 408 414 428 430 433-435 454 476 494 503-505 517-518 528 534 544 552 561-563 567 578 581 608-609 630 632 637 644 650 661 665 672 702 707 710 721-722 750 753 778 782 794 814 820 826 834-837 847 849-850 858 861 874 879 893 898 904 911 918 921-922 926 946 948 972 978 986 996 1020 1027 1031 1034 1053 1063 1068 1070 1073 1086 1089 1093 1097 1113 1119 1156 1159 1195 1198-1199 1208 1220 1227 1241 1261 1272-1273 1277 1285 1308 1315 1320 1324-1325 1330 1362-1363 1375 1403 1408-1409 1415 1431-1432 1435 1467 1469 1482 1504 1524 1542 1547

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1550 1567 1578 1581 1583 1594 1597 1601-1602 1611-1612 1615 1618-1619 1621 1625 1637 1645 1647 1652 1654-1655 1660 1666 1669-1671 1684 1706 1722 1737-1738 1742-1744 1760-1761 1763-1765 1772 1774
adult liver	Clontech	ALV003	29 676 997 1063 1119 1536 1766
adult ovary	Invitrogen	AOV001	1 4-18 20-23 29 35-40 42-48 50-51 53-58 61-63 65-66 68-69 73-75 77-78 80 82 85 87 89 97 100-101 103-104 106-108 110 113 115 118 122-124 126 128 133-134 136-140 142 145-147 149-157 161 166 168-170 174 177-178 180 182-186 188-189 192-203 207 209 211-215 219 221-224 229-230 234 242-243 246-247 255 258 260-262 265-269 271-272 274 277-281 284-286 288 290 295 299 301-302 304 307 309-311 313-314 316 321 323-326 330 332-333 335-338 341 344 349 352-353 356 358 360 362 370-372 376-377 379-384 387 390-392 394 397-398 400 403 408-410 412 414-416 423-424 426-427 430-435 439 443-446 448-449 451 453-455 462-463 468-471 473 476-479 481-484 487 489-494 496-497 499-501 503-505 509-514 516-517 519-520 522 524 526 528-534 541-544 546-547 549 552 554-555 561-564 566-567 569-570 572-573 575-576 579 581 583 585-588 590-591 593 595 597 599 601-605 607-613 615 618-622 624-627 630 632-633 636-640 642 644-647 649-652 654-655 657-665 667-675 677-678 681 683-684 692-695 697-710 714-721 723 725-727 729 732 734-735 743-746 750-751 753 758 763 765 767 772-773 775-778 780 783-784 786 788 790-791 794-796 800 803 805 809-811 813-815 818-819 821-824 826 828-829 831-832 837-838 843-850 852-857 859-864 867 869 871-872 874-875 878-883 887-888 890-895 898-910 912-914 916 919-922 924 926-927 929-939 941 943-946 948-951 953 955-958 961-964 966-967 970-979 981-982 985-986 988-990 992 995-997 999-1001 1004-1009 1011-1013 1016 1019-1020 1024-1025 1029-1031 1033-1035 1037 1039 1041-1047 1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217-1219 1221-1226 1232-1235 1238-1241 1243-1244 1247 1249 1252-1254 1256-1258 1262 1265 1267-1268 1270 1275 1278 1280-1283 1286-1289 1291 1293-1294 1298-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1299 1306 1308 1312 1317-1321 1323 1327 1329-1330 1332-1333 1338-1339 1341 1343-1351 1356 1359 1361 1365-1366 1371-1375 1377-1379 1383-1384 1386 1389 1394 1400 1404 1416-1417 1422-1427 1429-1431 1435-1436 1439-1443 1445-1450 1453-1454 1459 1463-1464 1466 1468 1470 1474-1481 1484-1485 1488 1491 1493-1494 1496-1498 1501-1504 1506-1507 1511-1517 1519 1521-1524 1526-1527 1530-1531 1534-1536 1538-1539 1541 1546 1548-1550 1553 1555-1559 1561-1563 1566-1567 1569-1570 1572 1574-1575 1578 1580-1581 1587-1588 1590-1591 1595 1597-1598 1600-1606 1609 1611-1621 1623-1630 1634 1636 1638 1641 1643 1645 1647-1657 1659-1662 1664 1667 1669-1671 1673-1674 1676-1681 1683-1690 1699 1702-1707 1710-1711 1713-1714 1716-1719 1723-1724 1726-1728 1731-1733 1735 1737-1738 1740-1741 1743-1744 1748-1751 1753 1755-1756 1760-1762 1765 1767-1768 1770-1771 1776 1778-1779 1783-1784 1786
adult placenta	Clontech	APL001	5-8 44-45 90-91 107-108 159 178 311 351 414 476 503 545 574 624 536 719 755 773 860 890-891 924 947 955-956 962 990 992 1002 1045 1202 1320 1369 1628 1686 1713-1714 1743-1744
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490-491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857-858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776
adult spleen	GIBCO	ASP001	3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386-387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744 746 762 765 774 780 788-789 794 810-811 817 822 830 832 845 848 852-853 858 862 866 874 879 882

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			884 906-908 912 919 921-923 926-927 934 942 949 957-958 963 977-978 983 990 992-994 996-997 999 1005-1007 1010 1012 1031 1036 1042-1044 1046 1049 1059 1068 1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1163 1170 1174 1177 1190 1196 1219-1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1353 1359-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782
testis	GIBCO	ATS001	5-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 522 526 547 552-553 563-564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779
Genomic DNA from BAC 63I18	Research Genetics (CITB BAC Library)	BAC001	686 1352 1412
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC002	1411-1412

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC003	1352
adult bladder	Invitrogen	BLD001	5-8 17-18 22-23 33 37-39 56-57 80 93 100 120-121 169 201 237 251-252 272 278 311 348 363 382 413 415 424 430 443 483 502 542-543 562 564 607 616-617 626 635 652 667 671 710 727 755-756 762 773 786 788 837 840 866 893 898 909 918 929 966 977 983 1016 1025 1055 1073 1082 1140 1167 1185 1189 1199 1270 1369 1481 1536 1560 1573 1596 1614 1636-1637 1649-1650 1654-1655 1658 1669 1671 1690 1719 1727 1731-1732 1739 1741 1760-1761 1779
bone marrow	Clontech	BMD001	3-8 11 13 18 29-31 33 35-36 40 43-45 47-48 50-51 57 60 65-66 75 80 82 85 88-89 94 100 103 107 110 115 118-119 124-125 133-134 136-137 139-141 146 150 152-153 155 161 163 168-170 172 178-180 187 192-193 197-198 203-205 210-213 215 217 219 222 224-226 233 235-237 242-244 255 258 260 263-264 266 273 276 278 283 286 290 295 301-302 307 312-313 321 330 333 339 343 352 357-358 370-371 382 384-385 387 389 394 408 410 412 416 421 424-427 429-431 436-437 439 441-442 445 447 454-456 461-462 471-472 475 477-479 481-482 485 488 493 498 500 503-506 513 516 519 523-524 526 530 535-540 542 544-545 549 555 565 567 569-577 581 583-586 588 593 601 603-604 608-609 613-619 621-622 632-633 636-637 642 649-650 656-660 666 670 672 674-675 679 683 701 708 716 718-720 731 735-736 740-742 744-745 752 761 765 772-773 775-778 780 785-786 789-791 796 798 802 810-812 823-824 826 830 832-833 837-838 843-844 848-855 858-859 866-867 869 878-880 883 890-892 896 903 905 908 912-914 922-924 927 930-931 937 939-941 952-953 955-958 963 969 973 976 981 985 987 990 992 995 1000 1002 1005-1007 1013 1016 1025 1028-1031 1033 1035 1037 1039 1042 1044 1047 1050 1053-1054 1059 1061 1063 1066 1070-1071 1079 1106 1110-1113 1115-1117 1124 1126 1134-1135 1142 1144-1145 1163 1172 1178 1197 1199-1200 1202 1216-1217 1224 1227-1228 1240 1246 1254 1261 1266 1270 1278 1281 1285 1287 1290-1291 1293 1299-1301 1308 1314 1317-1320 1327 1331 1339 1343 1346 1349 1353 1356 1361 1367 1369 1372-1374 1379-1380 1394 1400 1403 1406 1408 1413 1417 1419 1423 1425-1427 1430-1431 1433 1439 1443 1446-1449 1459 1463-1464 1482 1486 1493-1494

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1506 1509 1513 1521-1522 1524 1526 1528 1531 1536-1537 1543 1546 1548-1549 1552 1554-1555 1557-1559 1571-1572 1581 1589-1592 1597-1600 1609 1614 1621 1626-1628 1630-1632 1634 1636 1638-1639 1641 1646-1647 1651 1653-1655 1661-1662 1676-1681 1684 1686 1690 1702 1707 1711 1713-1714 1717 1720 1722-1723 1727 1737-1738 1740 1758 1767 1772 1781-1782 1785-1786
bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75 83-84 93 99 103 108-109 118 137 139 169-170 174 177 180 190 193 212-213 219 222 225-226 232 237 255 259 264 273-274 284 286 290-292 295 301 303-304 307 312-313 316 324 326 330 334-335 348 352-353 357 360 370-373 384 386-387 397 403-404 414-416 421 425-427 429-430 433-436 440 444 451 454 465-466 472 475 478 491 493 516 520 523 525 531 545 548 552 566 569-570 581 583 590-591 597-598 601 616-617 621 641 650 652 656 659 671 674-675 679 684 710 718-719 728 734 737-738 742 761 765 774-778 790 811 814 818 830 834-836 854-855 859 866 869 871 878-879 884 889 892 904 922-923 932 990 992 998 1001 1004 1016 1036 1042 1048 1051 1054-1055 1058 1088-1089 1106 1112-1114 1155 1157 1192 1200 1223 1227-1228 1236-1237 1260-1261 1282-1283 1285 1287 1295 1314 1317-1321 1324-1327 1330 1333 1341 1343 1347 1350 1353 1355-1357 1367 1369-1370 1373 1377 1379 1381 1383-1384 1394 1397 1400 1406 1413 1417 1425-1427 1438 1442 1446 1459-1460 1470 1493 1505 1521 1536 1546-1549 1560 1573-1574 1578 1598-1600 1621 1626 1631 1634 1646 1649 1653 1656 1658 1669-1670 1683-1684 1687-1688 1690-1693 1696 1699 1702 1704 1707-1709 1711 1720 1722-1723 1725 1727 1729 1731-1733 1738-1740 1743-1746 1752 1755 1760-1761 1767 1777 1781-1782 1786
bone marrow	Clontech	BMD004	73-74 503 922 1036 1711
bone marrow	Clontech	BMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLN001	17 56-58 103 110 117 144 150 171 179 185 188-189 201 204-206 210 218-221 225-226 231 237 251 277 288 310 312 320 333 359 386 388 394 408 420 455 481 485 503 510-512 590-591 615 635 647-648 665 672 684 697 710 725-726 743 780 786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953 976 983 993 1005-1006 1017 1020 1025 1027 1054-1055 1063 1068-1069 1140 1153 1170 1185 1196 1199 1220 1280 1314-1315 1320 1345 1351 1355 1369 1428 1439

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1462-1464 1512 1556 1583 1587 1594 1596 1614 1625-1626 1631 1639 1645 1650 1675-1677 1687-1688 1701 1713-1714 1724 1740 1765
Mixture of 16 tissues - mRNAs	Various Vendors	CTL016	401 1490 1686
Mixture of 16 tissues - mRNAs*	Various Vendors	CTL021	312 782 1132-1133 1403 1712 1715
adult cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33 37-39 43 46-47 58 61 64-66 71 73-74 82 85 94 100 103-104 113 118 122 126 130 134 140 147 153-156 163 170 179 181 186 192 195-196 198 201-202 218-219 222 229-231 257 266 276-277 285-286 288 298 301-302 304 307 312-314 324 326 329-330 332 335 342 352 358 362 371-372 376 379 381-382 384 388 398 400 410 414 416 419-420 426-427 430-431 433-436 439 446 448 461-462 464 471-477 479 482-483 491 493 496 503 506 510-513 516-517 526 530 535 542-544 546-547 557 561 572-573 575-577 581-582 585-586 588-589 593-594 600 602 604-605 607-609 612 615-619 623 644 650 654 657-658 662-665 670 672 680 683 691-694 698 706 708-709 711 713 720-721 727 729 731-732 737 745-747 753-754 760 765 771 774-777 780 790 793 796 798 800 803 805 818 826 828 831-832 834-836 843 847-848 851-855 857-860 864-866 869 871 876 878-880 882 887 890-891 897 899-902 905-908 912-913 916 918-919 922 927 932 934-938 944 948 955-956 958 963-964 967 969-970 972 976 978-979 983 985 990 992 1000 1005-1007 1016-1017 1024 1027 1033 1036 1038 1045 1047 1053-1056 1066-1067 1071 1073 1075 1079 1082 1098 1113 1124 1129 1134 1139 1146-1149 1163 1167 1170 1173 1175 1177 1181 1197 1200 1202 1211 1214 1216 1221-1222 1225 1227 1232-1234 1240-1241 1243 1258 1264-1265 1268 1270 1279 1287-1290 1308 1310-1311 1316 1320 1323 1327 1345 1349 1353-1354 1360 1372-1374 1383-1384 1386 1394 1397 1405-

*The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1406 1416 1425-1427 1431 1436-1437 1442 1446 1448 1453 1459 1466 1472 1478 1482 1496 1501-1503 1506 1512 1522 1527-1528 1531 1533 1541 1547 1569 1571 1585 1589 1597-1598 1600 1608-1609 1614-1616 1620 1623-1624 1626-1628 1630 1638 1641 1643 1649 1653 1656 1662 1667 1669 1671-1675 1683 1685-1688 1690 1702 1709-1710 1715 1717 1722 1724 1729 1731-1732 1735-1739 1741 1743-1744 1748-1749 1758 1760-1762 1767 1773 1778 1785-1786
diaphragm	BioChain	DIA002	137 282 289 730 780 986 1409 1478 1599 1614
endothelial cells	Stratagene	EDT001	3 5-10 13 15-21 24-26 29 34 37-39 42 44-45 50-51 53-55 57-58 60-61 65-66 68-69 73-74 77-78 80 82-83 85 87 89 93-96 101-105 108 110 112-114 116 118-122 124 128 133-134 137-142 147-150 152-153 161-163 166-172 176-179 187 190 192 194 196-201 204-207 210 212-214 220 224 229-230 233 235-236 240-241 251-252 258 261-262 265 267-269 272 276-277 279-281 284-285 288 290 295-296 301-302 310-311 313 316 321 325 329 331-333 335 340-342 351-355 360 371 375 380-382 384 387 390 392 397 400 407-408 410 412 414 416 425-427 431 434-436 439 444-445 449 454 463-464 472-475 477-479 486 488-490 497-498 500-504 510-513 516-519 522 524 526-528 532-534 536-540 542-546 548 561-563 566-567 572-576 579 581 585-586 589 593 595 597 599 603 607-612 615-617 620 622 626 630 632-634 638-641 644 647 656-660 662-664 670 673 678 680-682 692-697 707 709-710 712-713 719 730 732 734 736 738 743-746 751 759 768 771 773 775-778 783 786-789 793 800 803 805-807 810-811 814 816-818 821-822 824 826 828-829 832 834-838 842-845 848-850 854-860 862 864 869 871 874 876-879 883 885 887 890-891 894-895 898-900 903 908 910-913 916 919-922 924 926-928 930-935 939 943 948-949 951-954 957 959-961 964 969-970 973 975-978 983-984 988-990 992-993 996-997 1000 1002 1004-1013 1016-1020 1022-1025 1028 1031 1033-1034 1038-1046 1050 1055-1056 1059-1060 1062-1064 1067-1070 1072-1074 1076 1078 1082 1086-1087 1089-1090 1093-1097 1099-1103 1107 1109-1113 1116-1117 1124-1126 1128-1131 1134-1135 1138 1140 1144-1145 1148-1149 1153 1157 1160 1163 1171 1183-1184 1198-1199 1202 1205-1207 1211 1216-1217 1219 1221 1225 1229 1232-1235 1238-1241 1243-1244 1246 1250 1253 1257-1258 1261

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1265-1266 1268 1270-1271 1274-1277 1280-1283 1285-1286 1288-1290 1293 1295 1298 1308 1312 1317-1320 1324-1325 1327 1329-1330 1334-1335 1338 1342-1343 1345-1347 1350 1355-1356 1359 1367 1369 1374 1376 1379 1398 1400 1406 1408 1414 1417 1419 1424-1426 1428-1431 1434-1438 1440-1442 1448 1450 1462-1466 1468 1472 1474 1478 1487-1488 1491-1493 1501-1504 1506 1509 1511 1516 1520-1521 1526 1529 1531 1536-1537 1539-1540 1546-1547 1549 1552 1555 1557-1559 1561-1565 1568 1571 1575 1578-1579 1581-1583 1587-1588 1590 1592 1597 1605-1606 1611 1613 1615 1618-1621 1624-1628 1630-1631 1634 1636 1638 1641 1643-1650 1652-1659 1664 1666-1667 1669 1671 1675-1681 1683-1688 1696-1698 1703 1711 1715-1716 1719 1722-1723 1726 1731-1733 1736 1739-1741 1743-1744 1749 1755 1760-1761 1765 1767-1768 1771-1773 1776 1779 1783-1786
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	286 686 1297 1303-1304 1352 1411-1412 1754
esophagus	BioChain	ESO002	131-132 261 289 380 503 860 892 1000 1007 1397
fetal brain	Clontech	FBR001	62-63 89 112 126 194 322 336-338 379 391 411 481 546 563 607 679 710 867 1012 1031 1055 1251 1262 1320 1407 1643 1652 1686 1731-1732 1746 1765
fetal brain	Clontech	FBR004	68-69 90-91 139 212-213 301 331 362 374 403 436 611 645-646 659 668 670 691 785 805 845 1163 1209 1216 1232-1233 1238-1239 1387 1410 1416 1430 1496 1536 1547 1593
fetal brain	Clontech	FBR006	5-9 25 43 60 62-63 65-66 70 72 80 87 92 101 103 108 114 136 139 149 152-153 157 168 171-172 175 207-208 210 212-213 221-226 237-238 251-253 266 272 279-281 295 301-302 307 310 317-318 321-324 330 333-334 336-338 346-347 352 357 370 373 377 379-380 382 384 391-392 397 399 402 406-408 410-411 417 421 424 426-427 430 436-437 440-443 454 460 464 467 473 476 483 488-489 495 497 508 510-513 516 519-520 524 530 537-540 544 547 550 561 567 572-574 582 590-591 595 597 604 607-609 615 623 628-629 631 634 638-640 655 657-658 660 665 669 674-675 679 689 691-694 696-697 699 701 706 710 716 720 728 732 734 736 742-744 757-760 763 775-778 780 799 806-807 810 817-818 826 839 843 858 861 864 871-872 884 890-891 894-895 898 904 915 921-923 935-936 938 945 950 952 955-956 958-959 961 963 967 969-971 990 992

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			999 1001 1005-1006 1008 1013 1016 1022 1024 1029-1030 1032 1035 1042 1047-1048 1052 1056 1065 1067 1070 1082 1089 1109 1114-1115 1119 1131 1143-1149 1151 1153-1156 1160 1163 1167 1172-1173 1178 1184 1186 1188 1190-1200 1211 1216 1222-1223 1226-1227 1229 1231 1236 1245 1253-1255 1258 1260 1262 1266 1270-1273 1281 1287 1308-1309 1314 1317-1320 1326 1334-1335 1339 1341 1344 1350 1356 1369-1371 1373 1376 1379 1381-1382 1386 1392 1396-1398 1419 1423 1425-1426 1428-1429 1432 1437 1440-1441 1448 1466 1470 1482 1502-1503 1507 1511 1513 1516 1519 1536 1544 1549-1550 1557-1559 1573 1589-1590 1598 1608 1611-1614 1619 1621 1625-1626 1640 1651 1657-1658 1676-1679 1693 1696 1703-1704 1713-1714 1718 1720 1722 1724 1726 1728 1730-1733 1735-1736 1738-1739 1742 1745 1755 1759-1761 1765 1767 1771-1772 1777 1779-1780 1786
fetal brain	Clontech	FBR003	235-236 520 864 1068 1188 1587
fetal brain	Invitrogen	FBT002	15-18 20-21 24-25 29 34 43 61-63 77-78 98 101 103 107-108 128 130 136 146 148 165-166 171 174 181 185 196-198 204-205 208 223 230 235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
fetal heart	Invitrogen	FHR001	105 124 180 289 864 1036 1148 1229 1614 1616 1762 1785
fetal kidney	Clontech	FKD001	5-8 11 40 47 57 65-66 82 85 102 124 163 171 216 222 224 235-236

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			258 277 280-281 307 310 314 330 371 387 392 395 403 422-423 431 436 443 455 469 500 519 522 542 563 572-573 585 600 619 623 650 654 657-658 660 679 719 731 780 798 821 833 844 854-855 857 864 868 878 911 929 958 960 969 990 992 1007 1046 1087 1103 1129 1139 1285 1312 1331 1355 1369 1371 1376 1391 1422 1425-1426 1440-1441 1470 1543 1598 1601 1618 1631 1651 1654-1655 1669 1678-1679 1691-1692 1733 1785
fetal kidney	Clontech	FKD002	352 384 426-427 440 583 602 1060 1131 1324-1325 1636
fetal kidney	Invitrogen	FKD007	20-21 82 163 335 679 988-989 1000 1227 1230 1320 1554
fetal lung	Clontech	FLG001	35-36 94 323 371 398 426-427 445 473 549 560 604 616-617 626 631 649 651 719 746 786-787 832 842 849-850 864 894-895 1075 1178 1182 1200 1206 1309 1311 1345 1429 1493 1567 1576 1620 1686
fetal lung	Invitrogen	FLG003	9 15-16 29 41 47 68-69 83 88-89 102 124 137 152-153 165 196 224 229 231 249 254 256 267 291-292 300 325 333 344-345 352 373 376 379 384 408 426-427 430 432 467-468 475 483 488 493 516 531 535 545 547 549 564 582 602 623 644 660 662-664 670 673 725-726 728 761 765-767 774 805 830 852-853 864 875 921 932 937 946 949 963 988-989 1014 1016-1017 1024 1027 1090 1097 1170 1185 1200 1215-1216 1224 1258 1290 1309 1320 1342 1347 1355 1369 1381 1413-1414 1431 1438 1449 1491 1512 1536 1547 1557-1560 1567 1590 1601 1636 1644 1653-1655 1662 1667 1671 1675 1680-1681 1706 1739 1760-1761 1769
fetal lung	Clontech	FLG004	103 276 334 465-466 737 843 1131 1614 1658
fetal liver-spleen	Columbia University	FLS001	3-11 13 15-21 25 30-39 41-48 50-51 54 56-58 60-66 68-69 72 75 77-80 82-83 85 87 89 92-103 105-110 112 116-124 126-127 130 133 135-139 141 144 147-149 152-153 157 163-165 167-172 174 176-178 180 186 188-190 193-194 196 198-200 202-206 210-214 219 221-231 233-236 240-244 246-247 250-251 255-256 258 261-265 268-269 272 274 276-278 280-281 284-286 288 293 295 299-301 304 306-307 309 311 314 316 318 320-321 326 329-332 342 344-345 350 352-353 356-358 360 362 370-374 376 378-384 386-387 390 392-393 400-401 403 406 408 410-412 415 417 419 422-437 439-442 444-445 448 452-454 456 459 461-470 472-479 481-483 487-488 490-491 493 500-501 503-506 509-513 515-520 522-524 526-529 531 534 536-540 542 547-549 553-554 561-562 564 567-568 571-576 579 581 583 585-597 599-605

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			607 610-611 615-621 623-624 626 628-634 636-640 644 647-650 655-660 665 669-670 672 674-675 678 681-682 684 690-695 697 702 708-710 713-714 716-719 725-728 730-731 734 736 738 740-741 743-746 748 750-751 759-766 768 772 774-777 779 783-788 793 796 798 800-805 808 810-812 814 818-819 821-824 826-832 834-837 843-847 849-867 869-876 878-883 887 889-895 897-898 902 904-914 916 919 921-928 930-937 939 945-950 953-958 960-961 963-965 967 969 971 974-978 980-983 986 988-990 992-993 995-997 1000-1002 1004-1008 1012 1014 1016-1019 1025-1026 1028-1031 1033 1035-1036 1039-1044 1047 1049-1050 1053-1056 1058-1059 1061-1064 1067-1070 1072-1074 1076 1078 1082 1085-1087 1089-1090 1097 1099-1103 1107-1113 1115-1119 1121-1123 1125 1127-1128 1131-1134 1136-1137 1144-1150 1153 1159-1160 1163 1170 1175 1177-1178 1188 1190-1192 1195-1200 1202 1206 1208-1211 1214 1216 1218 1221-1222 1225 1227 1234 1237 1241 1244 1246-1247 1251 1254 1258 1261 1266 1268 1270-1273 1277-1282 1284-1285 1287-1290 1294 1299-1300 1306-1308 1313-1320 1324-1325 1327 1330 1332-1333 1338 1341 1343 1345-1347 1349-1350 1353-1360 1362-1363 1365-1367 1369-1370 1372-1374 1376 1378-1381 1383-1384 1386 1389-1391 1400 1402-1403 1405-1410 1413 1415 1417-1419 1422-1429 1431 1435-1437 1439-1442 1445-1446 1448-1449 1454 1458-1459 1466-1470 1472 1474 1477-1478 1480 1482 1485 1491-1493 1496-1498 1501-1507 1509 1511-1512 1516-1519 1524-1526 1529 1532 1536-1541 1546-1547 1549-1550 1552-1554 1562 1564 1569 1572 1574-1575 1578 1581 1583 1587-1588 1591-1592 1594-1595 1597-1598 1600-1604 1611-1612 1614-1615 1617-1618 1620-1622 1624-1625 1627-1628 1630-1632 1634-1639 1645-1651 1653-1662 1664 1667-1669 1671 1673-1674 1676-1688 1690 1696 1701-1703 1706-1709 1711 1713-1714 1718-1719 1722 1724-1727 1731-1733 1738 1740-1741 1743-1744 1746 1748 1751-1752 1754 1760-1765 1767-1773 1780 1783-1786
fetal liver-spleen	Columbia University	FLS002	3-11 13 15-21 26 29 32 35-39 42 44-45 48 50-51 54-55 57-58 61 64 68-69 73-75 78 80 82 84 87 95-98 100 103 105 107-108 110 112-113 116-119 122-125 128 130 137-138 145 147-153 155 157 159 161-163 166 168 171-172 174-175 177 181 188-189 193-194 196-198 200-203

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			206 212-215 219-221 223 225-229 231-232 240-244 246-247 250-251 258-259 262 264 268-269 272 275 277 280-281 284 286 288 290-292 295 298-299 301-304 306 308-310 318 320-321 323 325 329 331 334 342 348-349 352-353 356 359 368 371 374 376-379 381-384 386-387 392-393 397-398 400-401 403 410-413 421 423 426-427 429-430 433-436 438 440 443 445 448 451-452 454-455 460-463 465-467 469 471-473 475-476 478-479 481-483 487 490-491 493-494 497 500-501 503-505 509-513 515-517 519-520 524 526-531 534 537-542 544 547 552-554 556 558 561-562 564-567 571-577 583-587 590-591 593 595 597 601 604-606 608-613 616-617 619-624 626-632 634 637-642 644 647 649-652 654-659 662-665 669-672 674-675 681-682 685 688 690 696 698 700-703 707 709-710 713 717 719-721 723-724 728 731-732 734 737-738 742-745 748 752 754 759 763-766 768 770 773-777 780 782 784 786 791 795-798 801-802 805 808 811-812 818 823-824 826-827 832 834-837 839 843 846 848-856 858-861 865 867 869 871 873-874 876 878 881-882 887 889 892 894-898 901-902 904 906-908 913-915 919 921-924 926-932 934-935 937 939-941 943 946-947 950 953 958 961 965-967 971 973-975 977-979 981 984-985 990 992-993 995-997 999 1001 1004-1007 1009-1011 1013 1016 1020 1023 1025 1027-1031 1033-1035 1039-1042 1044-1045 1049 1053 1055-1056 1058-1059 1062 1064-1065 1067-1070 1072-1074 1079 1082 1087 1089 1093 1097 1099-1103 1105-1107 1109-1114 1123 1125-1127 1132-1134 1140 1143-1145 1148-1150 1156 1158 1160 1163 1172-1173 1177-1178 1181-1184 1190-1192 1195-1197 1199 1204 1206 1208 1211 1214 1216 1219 1227 1230 1234-1235 1237 1240-1241 1243 1245 1247 1256 1258 1260-1261 1264 1268 1270-1271 1275 1278-1279 1284-1286 1288-1289 1299-1301 1306 1308 1312 1314 1317-1319 1323-1325 1327-1330 1334-1335 1339 1343-1347 1349-1350 1354-1355 1357 1360 1362-1363 1365-1367 1369 1372 1376 1378-1380 1386 1389-1391 1394 1400 1403 1406 1409 1416-1419 1422-1427 1429 1435 1437-1438 1440-1442 1446 1448-1450 1453 1460-1461 1468 1470 1472 1474-1475 1478 1482 1486 1490-1493 1496 1498 1500-1504 1506 1508-1509 1511-1512 1516 1518-1519 1521 1524-1528 1531 1536-1538 1543 1547 1550 1554 1556 1564 1567-1569 1580 1587-1588 1591-1592

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1597-1598 1600-1601 1611-1612 1618-1620 1630-1631 1635-1638 1641 1646-1649 1652 1654-1659 1661-1662 1664 1667-1669 1674 1676-1679 1683-1684 1686-1688 1691-1692 1699 1702 1707 1711 1713-1714 1717 1719 1722 1726-1727 1730-1733 1738 1740 1743-1744 1748-1752 1758 1760-1761 1763-1764 1767 1769 1772-1773 1776 1779 1783-1786
fetal liver-spleen	Columbia University	PLS003	103 300 318 321 352 372 379 381 384 392-393 403 422 424 429 434-435 440 444 453 503 515 544 552 978 1064 1324-1325 1327 1333 1357 1369 1378 1418 1424 1622 1646 1649 1680-1681 1689-1690 1717 1743-1744 1769
fetal liver	Invitrogen	PLV001	15-16 26 34 58 61 64 70 75 78 89 98 105 112 116 120-121 123 133 151 166 176 180 194-196 198 200 204-206 210-211 220 225-226 230 235-236 239 247 259 261 267 272 277 280-281 303 310 313 317 320-321 329 344 356 371 374 376 379-382 395 408 412 414 419 429 434-435 441-442 465-466 490 494 504-506 509 522 527 534 552-553 562 567 569-570 572-574 607 631 657-658 667 669 672 685-686 702 717 725-726 732 748 759 761 778 784 786 809 817 829 837 857 861 872-873 875 881 889 894-895 909 911 916 954 963 967 974 977 986 988-989 993 995 997 1000 1005-1006 1008 1014-1015 1020 1042-1043 1070 1086-1087 1089-1090 1118-1119 1122 1144-1145 1148 1153 1157 1159 1183 1195-1196 1227 1250 1257-1258 1262 1267 1280 1285 1307 1312 1314 1317-1320 1344-1345 1349-1350 1355 1362-1363 1403 1405 1415 1419 1425-1426 1429 1431 1442 1448 1463-1464 1469-1470 1489 1528 1536 1539 1549-1550 1557-1562 1577 1583 1598 1601 1611 1615 1622 1644 1649 1666 1674 1706 1721 1738 1746 1763-1765 1774 1776 1779
fetal liver	Clontech	FLV002	676 998 1719
fetal liver	Clontech	FLV004	93 133 214 301 355 374 379 585 581 601 679 837 847 859 1123 1236 1270 1313 1324-1325 1327 1355 1367 1425-1426 1536 1690 1733 1760-1761
fetal muscle	Invitrogen	FMS001	26 37-39 50-51 58 84 86 89 98 113 128 131-132 139 155 172 186 194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715 725-726 730 733 761 775-777 788 826 837 860 874 913 915 921 935 970 980 986 988-990 992 1000-1001 1007 1014 1027 1035-1036 1045 1060 1064 1070 1083 1097

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1099-1102 1116-1117 1121 1164 1173 1198 1208 1228 1240 1258 1266 1270 1277 1298 1317-1320 1324-1325 1329 1336-1337 1369 1383-1384 1399-1400 1403 1409 1433 1505 1514 1542 1551 1554 1557-1559 1562 1589 1599 1620 1632 1644 1650 1652 1671 1675 1712 1725-1726 1743-1744 1754 1766
fetal muscle	Invitrogen	PMS002	119 221 273 402 426-427 463 547 599 736 869 1000 1033 1083 1266 1431 1440-1441 1468 1545 1599 1673 1678-1679 1687-1688 1710 1712-1714 1723 1725 1731-1733 1743-1744 1760-1761 1767
fetal skin	Invitrogen	FSK001	1 4-11 15-16 20-23 25 29 33 40 43 46 56-57 60-61 64-66 75 82 87 97-98 105 107-108 113 118-119 123 133 135-137 139 144 146 148 151-153 156 163 170 176 180 188-189 197-198 200 202-203 210 218 222 231 246-247 261 263 265-270 277 285-286 290 293 299 301 307 311 321 325 328 330 333-335 339 341 345 351-352 355-356 358-359 362 368 370 372 376 379-382 384 388 394 404-405 408-409 411-412 419-420 424 426-427 436 441-442 445 448-449 454 462 465-466 472 476 490 493 504 506 509 515-517 519 526 531 537-540 547 549 560-561 567 572-573 581 584 589 611-612 615 623 630-631 635 647 649 651 657-658 660 662-665 667 669 672 676 678 681 688 701 704-705 709-710 713 717 720-721 725-726 728-729 732 748 750 753 759 764 766 770 775-777 780-781 786 788-789 798 809 811 814 816-817 822 824-826 831 842 857 859 861 863-864 881 894-895 908 910-911 916 918 922-923 928 932-933 935 937 946 948-949 953 960-961 966-967 970 975 977 986 990 992-993 999-1000 1004 1007 1013 1018 1025 1027 1032 1035 1041-1043 1054 1057-1058 1060 1062-1064 1069 1072 1077 1090-1091 1097 1099-1103 1108 1113 1119 1123 1128 1131 1134 1140 1148-1149 1152-1153 1156 1163 1167 1178 1182 1189 1192 1195-1196 1198 1201-1205 1208 1211-1212 1216 1219-1220 1222 1225 1240 1243 1258 1266-1267 1274 1277 1280 1282-1285 1299 1310 1317-1322 1324-1325 1329-1330 1342 1344 1346 1349-1351 1354-1357 1365-1366 1369 1371 1373 1376 1378 1380 1383-1384 1387 1399-1400 1405 1410 1427 1429 1431 1433-1435 1439-1441 1448-1449 1454 1457 1468 1470 1472 1475 1480-1481 1487 1490-1491 1493 1498 1509 1512 1521 1525-1526 1529 1535-1536 1547 1549 1557-1559 1588 1592 1595 1597-1598 1601 1603-1604 1608 1611 1614 1618 1624-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1626 1632 1634 1636 1641 1643-1644 1646 1654-1657 1660-1662 1665 1668 1675 1685 1687-1689 1702-1703 1709-1710 1716 1719 1724 1727 1731-1732 1737-1740 1742 1747 1749 1755 1760-1761 1765 1772 1776-1777 1779-1780 1786
fetal skin	Invitrogen	FSK002	13 286 302 307 313 321 330 335 339 341 354 370 372 385 400 402 408 414 426-427 433 436 450 454 515 544 585 598 767 810 845 939 1076 1109 1155 1317-1320 1326 1333-1335 1343 1347 1350 1369-1371 1377-1378 1391 1397 1422 1466 1647 1656 1678-1679 1687-1688 1693 1718 1721 1725 1731-1732 1739 1755
fetal spleen	BioChain	FSP001	110 137 211 353 589 927 1108 1639 1771
umbilical cord	BioChain	FUC001	4-8 10 12 14 17 33-36 44-46 57 64 68-69 75 82 85 101 104 113-114 116 119 122-124 133 137 153-154 157 161 163 166-167 175 181-184 186 192 197-198 200-202 212-215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588-591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667-668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725-727 732 749-750 762 765 771 775-777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897-900 903 906-907 911-912 925 930-933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005-1007 1016 1023 1025 1037 1046-1047 1059 1061-1063 1073 1076-1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286-1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440-1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504-1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575-1576 1578-1579 1591 1595 1600-1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735-1738 1740-1741 1760-1761 1768
fetal brain	GIBCO	HFB001	4 9 11-13 17-18 22-23 25 37-39 42-47 50-51 54-55 58 60-61 65-66

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			72 75 77 80 82 85 90-91 94 100-102 107 110 112-116 118-119 122-123 126 128 134 136-140 147-148 153-155 157 161 165 169-172 175 181 186 188-189 197-198 204-206 208 210 215 222-223 225-226 230 235-238 240-241 247 253 256-258 260-262 267-269 276 279-281 284 286 289 298 300-302 307 310 318 321-323 325 330-331 339 341 346-349 352 354 356-359 362 364-365 371-372 377 379-380 382 384 387 390 400 408 414-416 419 424 431 434-435 438 441-443 449 451 453-455 457-463 470 472-473 475 477-478 482-483 486-488 490-491 493 496 499-500 502-504 506-507 509-512 516 519-520 522 525-526 529-530 537-540 543-544 546-547 566-567 569-570 572-582 585 588 590-591 593 595 599 601 604 606-609 611-612 614-620 622-624 630 632 636 643 645-647 650-652 654 659 661 665 667-668 670-672 676 678 681 687 689 692-694 697 699 710 714 717 721 727 729-732 734 736 738 743-746 750-751 759 763 766 770 772 775-777 784 789 791 796 799 802-805 810-811 814 819-821 824 826 830 834-837 839-850 854-856 858-860 862 864 869 871 876-877 879 883 886-887 890-891 893-895 898-901 905 908-910 912-916 919 922-923 925 927 930-933 935-938 948 952-960 963-964 967 969-972 975 978-979 981 983 986-987 990 992 995 997 999-1002 1005-1009 1011-1013 1016 1018-1019 1023 1026 1029-1031 1033-1035 1038 1041 1047 1050 1053 1057 1059 1064 1068 1070 1072-1073 1078-1079 1081-1082 1086 1089 1094 1097 1103 1107-1109 1113-1115 1121-1122 1127 1134-1135 1138 1140 1143 1148-1151 1153 1156-1157 1159 1167 1170 1175 1193-1194 1200 1202 1207-1209 1211 1216 1219-1220 1226-1227 1229 1232-1234 1240-1241 1243 1246 1249-1251 1253-1254 1258 1267-1268 1271 1276 1279 1282 1285-1289 1293-1294 1305 1307-1308 1312 1316 1320 1327 1338-1339 1341-1344 1346 1349 1355-1357 1359 1365-1366 1369-1370 1373-1375 1379 1386 1389 1394 1398 1409 1413-1414 1416-1417 1420-1421 1425-1427 1430 1433 1437 1439 1442 1445-1452 1454-1457 1459 1463-1464 1468 1470 1474 1477-1479 1489 1492 1494 1497-1498 1501-1503 1507 1509 1511-1513 1517 1520-1521 1524-1526 1531-1533 1535 1537-1538 1547 1554 1556-1559 1564-1567 1571 1584 1587 1589 1594 1599-1601 1611-1612 1614-1616 1619-1620 1625-1628 1630-1631 1634 1637-1638 1640-1643 1645 1648-1649 1651 1653-1655 1657-1658 1664-1665 1667 1669 1673 1678-1679 1683-1684 1686 1693 1701 1704-1705 1709 1713-1714 1717-1720 1724 1727-1728 1731-1733 1737-1738 1743-1744 1752 1754-1755 1757 1760-1761 1765 1772 1779 1785
macrophage	Invitrogen	HMP001	5-8 110 204-205 503 634 678 859 878 933 988-989 1379 1448 1504
Infant brain	Columbia University	IB2002	10 12-13 15-18 22-23 25 29 34 37-39 43 47 50-51 54-56 58 60-63 65-66 68-69 72-74 80 82-83 86 88-92 97 100 102-104 106-108 110 112-113 115-116 118 123 128 130 134-136 138-139 143 147-149 151-152 154-155 163 165-167 169 172-175 181-184 186 193-196 198 201 203-205 209-210 214-215 222 224-226 231-232 235-236 239 246-247 252 257 260 268-269 272 276-277 279-281 286 288 291-292 295 298 300-301 304 307 310 313 321-323 330-331 333-334 339 346-347 349 352 356-357 362 371-372 377 379-380 383-384 392 397 401 406 408 411 413-414 416 418-419 422 428 430-431 434-435 438 443 449 453-454 461 464-466 469-470 472-473 475-476 478 482-483 487 490 492 494 497 503 507-508 510-513 516 519-520 524-526 530-534 536-540 547 550-551 561 563-564 566-567 572-576 579 581-582 584-587 590-591 593 595-597 607-609 611-613 616-617 620 622-624 627 631 637 641 645-647 650-655 657-658 660-665 667-675 689 691 695 697 699 703 707 713-715 717 721 728-731 733-736 739 743 745 751 755 759 763 769-770 772 778 780-781 785 788-789 793-794 799 803 808 811 814 825-826 830 834-836 840-843 845 848-850 854-855 860 862 864-865 870 872 875-876 878 886 888 890-891 894-896 898 903-904 916-917 919 922-925 927-928 930-932 934-936 938 941 945-946 948-950 953-954 959-962 966-969 977 979 981 986-990 992 997 999-1000 1004-1006 1014 1016 1018-1019 1024-1025 1033 1036 1047 1051-1052 1054-1055 1057-1059 1063-1064 1068-1070 1073 1081-1082 1085 1089 1108-1113 1118-1120 1123-1124 1130 1132-1138 1140 1149 1151 1153-1154 1163-1170 1172 1174-1175 1183-1184 1188 1190 1193-1194 1196-1197 1199 1204 1208-1209 1211 1218-1222 1226-1227 1229 1231 1234 1241 1247 1249 1251 1256 1258 1261-1262 1269 1274 1279 1281 1283 1285 1287-1289 1294-1295 1305 1307 1313-1314 1316-1320 1329 1332 1341-1342 1345 1349 1356 1362-1363 1365-1366 1368-1370 1374 1381 1383-1384 1388 1400 1403 1406-1407 1413 1417 1420

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1423 1429-1431 1435-1436 1439-1441 1443 1447-1449 1451-1452 1454-1455 1457 1459 1463-1465 1468 1470-1471 1475 1479 1482-1483 1485 1493-1494 1496 1498-1499 1502-1503 1505-1507 1509 1522-1523 1525 1528 1531-1533 1542 1546-1547 1549-1550 1554-1555 1563 1565-1567 1569 1575 1580 1583-1586 1588 1590 1592-1593 1595 1598 1600-1601 1608-1610 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1658-1659 1664-1665 1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1717-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1755-1758 1762 1765 1771 1774 1777-1778 1786
infant brain	Columbia University	IB2003	17-18 20-23 29 34 43 60 68-69 78-80 88 100-101 107 110 112 118 123 128 133 135-137 146 148 152 159 166 169 174 194 198 203 215 223 225-226 229 235-236 247 260 276-281 286 290-292 295 300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572-576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674-675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144-1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778
infant brain	Columbia University	IBM002	101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779
infant brain	Columbia University	IBS001	10 12 119 175 279-281 321 334 371 446 551 563 623 652 667 669

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			671-672 819 949 966 1113 1130 1151 1188 1193-1194 1196 1229 1258 1265 1271 1287 1317-1319 1324-1325 1342 1423 1440-1441 1448 1471 1482 1525 1532 1546 1562 1569 1588 1591 1610 1618 1647 1649 1658
lung, fibroblast	Stratagene	LFB001	5-9 17 20-21 25 68-69 82 94 105 153 157 197-198 203 207-208 212-213 223 262 266 283 302 321 326 333 356 370 427 430 436 446 462 472 493 498 503 516 519 527 535 537-540 542-544 562-565 567 586 599-600 607 615 630 647 662-664 692-694 712 719 745 748 775-777 794-796 810 837 843-847 849 854-856 869 876 903 934 953 955-956 964 975-976 984 1000 1005-1007 1024-1025 1033 1039 1053 1064 1070 1072 1082 1112-1113 1134 1136-1138 1140 1195 1223 1232-1233 1246 1279 1285 1295 1311 1320 1334-1335 1343 1427-1428 1446 1478 1482 1493 1504 1537 1552 1555 1567 1575 1582 1598 1620 1625 1632 1638 1645 1654-1655 1662 1680-1681 1684 1686 1690 1696 1702 1711 1733 1741 1760-1761 1778 1785
lung tumor	Invitrogen	LGT002	5-10 18 20-21 29 33-36 40 43 52 54-55 61 65-66 68-70 73-75 80 85 88-89 93-94 100 103 106-108 112-113 115-116 118-119 123-124 126 130-132 135-137 139-141 143-144 147-148 151-153 155-156 159 161 164 169 171 179-180 185 190 192 194 196-199 203-208 210 212-214 216-217 219 222 233 240-241 244 246 251-252 255-256 261-262 266 272 276-277 279-281 284 286 288 290 295 298 301-302 309-312 317 321 329 332 341-342 344-345 348 352 358-360 363 368 370-371 376 380-381 384 389-390 398 400 409 414 423 426-427 430 432-436 443-444 450-451 454 462 468 472-477 480-483 487-488 490-491 493 496-498 500 503-506 509-512 515-516 519 521-523 526 530 534 541 544 547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787-789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841-845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932 934-935 937 947 950 953 955-956 961 963 966-967 969 971 977-979 981 984 986-987 990 992-993 995 997 999-1001 1005-1007 1009 1012-1013 1018 1020 1022-1024 1026 1029-1030 1033 1038 1041

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1045 1047-1050 1052 1054-1055 1059 1063-1064 1067-1071 1073-1074 1078 1085 1087 1089 1095-1097 1104 1106-1107 1109 1112 1116-1117 1119 1126 1134-1135 1139 1141-1142 1144-1145 1148 1152-1153 1156-1158 1167 1170 1172 1178 1195-1196 1198-1200 1202 1204 1208 1214 1216 1219 1222 1227 1234 1241 1247 1252 1257-1258 1265 1267-1270 1276 1278 1280-1281 1283 1285 1288-1289 1295 1300 1305 1308 1312 1317-1321 1329 1338-1339 1341 1344-1346 1349-1351 1353-1355 1357 1365-1366 1369 1378-1379 1383-1385 1394 1397 1400 1402-1403 1408 1417 1419 1423-1426 1431 1433-1436 1438 1444 1446-1448 1454-1455 1460 1466 1468 1470 1474 1480-1481 1483 1486-1488 1490-1491 1494-1496 1506 1508-1509 1511-1512 1515-1516 1519 1523-1524 1528-1529 1536-1540 1546 1549-1550 1555 1560-1561 1565 1567 1569 1575 1588 1591 1593-1594 1596-1598 1600-1602 1608 1614-1616 1618 1620 1624-1625 1627-1632 1636 1639 1644-1645 1647-1649 1652-1653 1656-1662 1664 1666-1667 1670-1671 1673-1675 1678-1679 1683 1685-1688 1690-1692 1696-1699 1705 1709 1716-1717 1722 1727 1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786
lymphocytes	ATCC	LPC001	4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188-189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325-326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426-427 430-431 445 447-448 451 454-455 475 503 516 526-527 530 537-540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906-907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1150 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269-1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428 1431 1437 1446 1448 1461 1466 1470 1472 1474 1482 1492 1506 1528 1537 1546 1549 1591 1598 1600 1603-1604 1606 1627 1636

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1638 1647-1649 1651 1658-1659 1664 1676-1677 1680-1681 1687-1688 1699 1711 1715-1716 1726 1728 1737 1740 1746 1748 1752 1756 1758 1777 1779
leukocyte	GIBCO	LUC001	3-4 10-11 13 15-18 20-21 24-25 30-31 35-36 40 43-45 48 50-51 54-58 60-63 68-69 75 79-80 82-83 85 88-91 93-96 98 100 103-104 107-108 112 116 119 123 125-128 134-140 142 147-149 151 153 155 157 162-163 167 169-172 174 177-179 186 190 192-199 203-207 210 212-215 217-219 222-223 229 235-236 247 251 255-258 260 262 272 274-277 280-281 285-286 297-301 307-310 313-314 316-317 321 325-330 333-334 340-342 348-349 352 354-358 370-371 380-385 387-388 400 405 408-410 412 414-416 421-425 430-431 434-435 437 439 441-442 445-451 453-454 456 459 461-464 468-472 474-479 481 483-485 487-491 496 499-501 503-504 509-513 516-519 522 526-527 529-531 534 536-540 542 547-549 553-559 566-567 571 574-577 579 582 584-586 589 593 595-597 601-602 604 606-607 611-613 615-621 623 627-629 633 636-637 642 644-650 655 659-660 662-665 667 669 674-675 678 682-684 692-696 698 700 706 708 710 716-720 725-726 729-736 738-739 743-746 749 751 753 756 759 765-766 768 770-778 780 784-786 788-790 793 796 798 800 802-803 810-811 814 817 819 826 828-830 832 834-836 838 843 845-860 863-864 866-871 877-879 881-892 894-896 898 902 904-914 916 919-925 927 930-932 935-936 941-942 945 948-949 953 955-956 958 960-962 964 967 970-971 973 975 977 985-990 992-993 995-996 999-1002 1004-1009 1011 1014 1017-1019 1022-1023 1025 1027 1029-1031 1033-1036 1038 1041 1043 1047 1050 1053-1054 1058-1059 1061-1062 1064 1068 1070 1072 1078 1085-1086 1089-1091 1093 1097 1106-1107 1110-1113 1115-1117 1122-1123 1125 1129 1132-1133 1135-1137 1140-1145 1152 1158 1163 1168 1170-1174 1176-1178 1180 1182-1183 1186 1195 1198-1200 1202 1205-1206 1211 1216 1219-1221 1223-1227 1230-1236 1238-1242 1247 1252 1254 1256 1258 1261-1262 1264-1265 1269-1270 1272-1275 1277 1280-1284 1287-1293 1299-1300 1306 1308 1312-1313 1317-1320 1322 1324-1330 1333-1335 1339 1341 1343-1347 1349 1353-1357 1359-1361 1365-1367 1369-1370 1373-1374 1377 1379-1381 1386-1387 1394 1400 1403 1409 1419 1423 1425-1428 1430-1431 1433-1434 1437-1438 1440-1442 1446-1448 1450

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1453 1458-1459 1463-1464 1468 1470-1471 1474 1477-1478 1482-1488 1490-1493 1496-1501 1504 1506 1509 1512-1513 1516 1519 1521-1522 1524-1525 1527-1528 1531 1534 1538 1541 1545-1547 1549-1550 1553 1555-1556 1560 1565 1567 1575 1580 1589 1591 1594 1596 1598 1600-1602 1606-1608 1611 1614 1620-1621 1624 1626-1629 1631-1632 1636 1638-1639 1641 1644-1645 1648-1650 1653-1655 1658-1660 1662 1669-1670 1675-1679 1684-1688 1690-1692 1696 1700 1702 1707-1709 1711 1716-1717 1720 1723 1725-1727 1733 1737-1738 1741 1743-1744 1748-1749 1752 1755 1760-1762 1765 1769 1771-1772 1781-1784 1786
leukocyte	Clontech	LUC003	4 35-36 44-45 61 68-69 75 82 102 119 139 154 179 197 244 280-281 324 372 404 430-431 455 461 476-477 481 503 537-540 554 575-576 581 589 608-609 621-622 624 630 632 647 662-664 669 679 698 764 773 775-777 802 848 851 856-857 879 905-907 915 949 952 990 992 1002 1113 1119 1170 1183 1216 1236-1237 1241 1275 1346 1353 1357 1359 1377 1506 1515 1534 1553 1591 1600 1613-1614 1621 1628 1670 1676-1677 1691-1692 1699 1733 1738 1772
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	25 35-36 43 80 104 126 128 150 163 166 188-189 197 210 215 220 271 277 280-281 310 317 336-338 345 351 372 380-381 383 387 412 415-416 430 445 448 454 456 467 481 490 499 503 526 528 546 548 567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1060 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669-1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760-1761
mammary gland	Invitrogen	MMG001	5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144-146 148 150-152 154 158-159 165-166 170-172 174 176 178 181-185 188-190 194-198 201-206 210 217-222 224 227-228 231 233-237 247 251 253-254 256 261-263 266-267 271 276-277 279-281 284-286 288

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			290 297 299 301 304 309-312 318 320-321 323-325 327-329 331-332 334 339 341 344-345 348 350 356 359-360 362-363 368 371 376 379-383 388 390 393-395 397-398 405 408 412 414-415 423 430 434-437 441-444 448 451-455 462-464 474 476 479 482 485-486 488 490 494-495 498 501 506 509-512 516-517 519-520 522 527 529 534 537-541 547 549 554 557 562 572-574 587 589-591 597 602 607 618 623 628-629 632 634-640 644 647-648 650-652 655 657-658 660 665 667 669-672 674-676 679 682 688 695-696 706-707 710 713 717 720 722-730 732-734 736 738 743 747-748 750 755 759 761 766 770 780 784 786-789 794 803 806-807 809 814 817-822 827-829 837 842 854-858 863-864 866 869-870 872 878 881 889 893-900 904 906-907 911 916 919 921-923 926 935-937 946 948-949 953-954 957 960-961 963 965-966 970 977-978 984-989 993-997 1000-1001 1005-1006 1008 1013-1014 1016-1017 1023 1025 1027 1032-1033 1036 1039 1043 1045 1055 1057-1058 1063 1068-1075 1077-1078 1085 1087 1089-1091 1095-1102 1107-1108 1112-1119 1121-1123 1131-1133 1136-1137 1139-1142 1144-1145 1148-1149 1153 1159 1167 1170 1172-1173 1183-1185 1190-1192 1196-1199 1207-1208 1212 1216-1218 1222-1223 1225 1231 1234 1240-1241 1247 1253-1254 1258-1259 1261-1262 1270-1280 1283 1285-1286 1298 1307 1314 1316-1320 1323-1325 1330 1334-1335 1342-1345 1349-1352 1354-1355 1359 1369-1370 1377 1379 1381 1383-1384 1389 1405 1414 1419 1421-1423 1425-1426 1428-1429 1431 1434-1437 1439 1448-1449 1454 1457 1460-1464 1466 1471 1480-1483 1487 1489-1491 1493 1505 1507 1512 1519 1526-1528 1532 1534 1536 1539 1542 1547 1549-1550 1554 1561-1562 1564 1567 1572 1576-1579 1581-1582 1587-1588 1592 1594 1596-1597 1601-1602 1607-1608 1610 1612-1616 1618 1621-1622 1625-1626 1631 1635-1636 1641 1643-1644 1647 1650 1652 1654-1655 1657-1658 1660 1662 1664-1666 1669-1671 1673-1674 1676-1677 1680-1685 1689-1692 1701 1706 1713-1715 1719-1720 1723-1728 1730-1732 1738 1740 1742-1744 1746-1747 1749 1751 1753 1760-1762 1765-1768 1771 1774 1776-1777 1779 1783-1784 1786
induced neuron cells	Stratagene	NTD001	29 35-36 80 116 123 156 163 181 214 230 280-281 284-285 307 321 330 340 358 371 375 377 380 382 422 424 492 497 532-533 542 546

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			549 566 586 595 612 645-647 654 734 775-778 780 792 799 821 826 856 858 875 936 953 985 990 992 1041-1043 1055 1072 1104 1193-1194 1206 1223 1246 1253 1274 1288-1289 1291 1294 1311 1320 1349 1359 1412 1423 1485 1620 1623 1645 1684 1705 1715 1751
retinoid acid induced neuronal cells	Strategene	NTR001	5-8 78 268-269 277 383 431 506 623 677 731 999-1000 1199 1425-1426 1547
neuronal cells	Strategene	NTU001	29 65-66 80 82 110 119 146 152 166 174 181-185 198 227-228 253 284 309 325 332 334 336-338 375 391 393 406 414-416 454 465-466 470 488 503 506 510-512 519 537-540 572-574 597 602 607 623 647 661 700 702 716 743 771 792 858 904 948 954 977 1000 1005-1006 1025 1064 1068 1122 1148 1185 1219 1226 1234 1246 1271 1283 1295-1296 1311 1317-1320 1329-1330 1350 1355 1365-1366 1378 1383-1384 1400 1412 1445 1505 1539 1547 1578 1647 1656 1683 1690 1738 1749 1783-1784
pituitary gland	Clontech	PIT004	311 314 379 408 419 430 454 1055 1095-1096 1272-1273 1312 1320 1378 1652 1671 1720 1725 1736 1741 1755
placenta	Clontech	PLA003	5-8 124 208 277 370 843 906-907 1280 1317-1319 1369 1609 1621 1737
prostate	Clontech	PRT001	9 46 57 71 107 147 171 177 197 201 229 231 242-243 274 280-281 307 310 317 330 358 373 382-383 400 430 434-436 461-462 469 477 489 497 500 505-506 513 521 526 531-533 547 618 649 657-658 662-664 710 729 767 771 789 820 861 871 874 890-891 905 938 945 963-964 988-989 1002 1025 1033 1045 1061 1095-1096 1112 1125 1142 1196 1198 1202 1232-1233 1241 1258 1272-1273 1287 1295 1313 1333 1341 1344 1349 1360 1362-1363 1367 1437 1442 1447 1475 1478-1479 1482 1489 1513 1517 1527 1531 1536 1598-1599 1628 1636 1657 1680-1681 1687-1688 1717 1738 1743-1744
rectum	Invitrogen	REC001	17-18 29 33 62-63 71 73-74 83 86 113 126 146 153 158 167-169 195 200 206 261 309 312 341 344 368 373 388 395 408 414 420 430 441-442 446 448 464 468 483 517 537-540 547 567 585 589 602 623 628-629 632 645-647 651 657-658 669 717-719 721 725-726 738 748 750 756 762-763 766 770 774 790 819 825 843 849 851 881 903 909 948-949 960 986 996 1020 1023 1033-1034 1064 1067 1070 1075 1086 1108-1109 1113 1130 1139 1153 1159 1172 1178 1185 1187-1189 1205 1220 1225 1240 1244 1271 1317-1320 1323 1334-1335 1350-1351 1355 1369 1373 1375 1425-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1426 1436 1439 1469 1474 1477 1482 1546 1587-1588 1592 1596 1610 1622 1627 1644 1658 1662 1665-1666 1669 1675-1677 1749 1786
salivary gland	Clontech	SAL001	10 55 97 103 110 140 149 152 158 198 217-218 242-243 256 301 308 312 321 333 351 354 360 410 437 448 473 487 494 496 501 535 555 569-570 572-573 590-591 624 636 651 759 762 764 768 771 788 800 809 826 848 865 879 906-907 925 933 963 1016 1020 1025 1040 1046 1055 1066 1103 1150 1172 1181 1234 1281-1282 1288-1289 1298 1315 1320 1333 1336-1337 1346 1359 1373 1379 1424 1447 1449 1474 1482 1492 1494 1498 1511 1523-1524 1537 1554 1596 1626-1627 1636 1652-1655 1658 1665 1671-1672 1691-1692
salivary gland	Clontech	SAL503	158 326 1423 1463-1464
skin fibroblast	ATCC	SFB001	1320 1400
skin fibroblast	ATCC	SFB002	262 736 1025 1253
skin fibroblast	ATCC	SFB003	709 1119 1350 1631 1653
small intestine	Clontech	SIN001	25 142 146-147 151 155 198 203 244 260 271 280-281 286 288 298 301-302 308 312 334 340 371 398 408 412 414 416 423 426-427 430 434-435 445 452 454 478 503 516 519 521 523 543 547 549 555 559 563 569-570 585 592 604 611 626 628-629 632 650 659 681 710 714 718 750 764 780 798 829 842 857 859 866 887 892 894-895 901 904 906-907 912 919 935 997-998 1000 1007-1008 1026-1028 1044 1055 1089 1097 1116-1117 1131 1148 1169 1199 1219 1234 1247 1264 1279 1316 1320 1326 1341 1343 1349 1351 1374 1387 1398 1400 1403 1407 1423 1428 1468 1498 1501 1521 1550 1556 1585 1597 1636 1638-1639 1645 1653 1656 1662 1671 1675 1684 1691-1692 1704 1711 1717 1719 1722 1725-1726 1729 1733-1734 1743-1744 1762 1767 1780 1785
skeletal muscle	Clontech	SKM001	18 20-21 82 84 101 118 134 148 151 153 166 225-226 258 274 277 289 329 361 412 414 424 440 452 459 470 488 503-504 537-540 647 660 673-675 715 773 780 786 830 905 922 950 963 982 990 992 1020 1047 1063 1115-1117 1121 1134 1228 1268 1284 1298 1321 1329 1336-1337 1343 1409 1413-1414 1509 1599 1624 1644 1653 1712
skeletal muscle	Clontech	SKM002	168 1683 1712
skeletal muscle	Clontech	SKMa03	235-236 1409
skeletal muscle	Clontech	SKMa04	235-236
spinal cord	Clontech	SPC001	4 9 11 17 30-31 35-36 43 46 60

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			82 85 92 94 108 110 116 139 157 167 198 204-205 210 215 229 256 259 277 280-281 300-302 304 315 317 372 379 387 392 419 426-427 430 433 448 467 473 487 489 506 509 513 519 524 526 537-540 543 547 549 551 559 567 569-570 593 607 616-617 623 625 637 649-650 652 657-658 670-671 673 679 681-682 709 711 715 719 728-729 734 749-750 753 775-777 781 789 791 809 820 832 834-836 847-849 854-855 858 861 864 871-872 875 884 898 906-908 917 919 924 934 942 944 970 985 990 992-993 998 1013 1039 1053 1059 1065 1072 1075 1077 1082 1085 1097 1103 1109 1116-1117 1128 1134 1151 1170 1174 1192-1194 1215 1225 1241 1243 1283 1294 1307 1312 1320 1323 1327 1330 1350 1353-1354 1356 1359 1368 1375 1400 1406-1407 1423 1429 1437 1443 1448 1454 1470 1482 1492 1501 1508 1511 1529 1538 1548-1549 1565 1571 1578 1598 1600 1614 1625 1627 1630 1639 1646 1651-1652 1670 1686 1696 1740 1751 1755 1771
adult spleen	Clontech	SPLc01	117 312 326 348 424 426-427 431 845 866 1320 1330 1333 1344 1355-1357 1371 1387 1397 1446 1538 1579 1669 1686 1739 1767
stomach	Clontech	STO001	10 15-16 61 68-69 100 117 149 197 201 227-228 231 249 273 280-281 287 291-292 302 312 358 362 426-427 430 446 462 475 479 535 597 620 630 651 662-664 722 739 780 782 785 846 919 960 964 966-967 976 1008 1012 1032 1042 1063 1071 1135 1170 1208 1234-1235 1259 1277 1280-1281 1322 1349 1359 1369 1449 1468 1474 1478 1487 1493 1498 1557-1559 1622 1634 1651 1653 1729
thalamus	Clontech	THA002	9 11 25 65 87 112 137 146 180 190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613-1614 1640 1651-1652 1671 1687-1688 1703 1743-1744 1746-1747 1753
thymus	Clontech	THM001	44-45 54 57-58 62-64 79 104 123 126 134 153 193 212-213 218 242-243 258 274 277 279 297 301 307 327 330 333 342 351 358 371 410 430 445 465-466 468 471 483 487 493 503 506 509 517 526 535 537-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			540 546 548 554 567 584 586 590-591 604 612 621 638-640 645-647 649 656 660 665 670 698 710 720 728 735 739 746 759 762 766-767 775-777 780 784-785 800 802 809 824 826 828 845 851 858-859 864 866 870-871 878 884 887 892 899-900 927 930-931 967 983 986 990 992 999 1014 1029-1030 1033 1059 1066 1073 1103 1107 1113 1116-1117 1119 1140-1142 1158 1163 1172 1177 1195 1206 1209 1213 1216 1218-1219 1221-1222 1227 1271 1277 1282 1320 1329 1349 1367 1369 1383-1384 1417 1419 1423 1425-1427 1448 1477 1488 1493 1536 1554 1620 1644 1646 1649 1654-1655 1661-1662 1669-1670 1674 1676-1677 1685-1688 1707 1711 1731-1732 1737
thymus	Clontech	THMc02	5-9 15-21 25 33 35-36 43-45 48 50-51 54-55 60 75 83 87 89 93 98-100 102 105 112 117 135-137 141 143 146 157 167 169 192 196 211 217-219 222 224 229 233 235-236 240-241 244 251-252 256 261-262 268-269 286 288 290 295 297 301-302 309-310 315-317 321 324 327 334 342 350 352-353 360 370-373 382 384 400 403 410 414-416 424 430-431 436 445 454-456 461 464-467 470 472 474-476 483 488 497 500 504 506 513 516 519-520 524 526 530-531 534 537-540 549 554-555 565-566 569-570 572-573 575-577 586-587 595 603-604 606 612 630-632 634 636 647 650 657-660 666-667 669 673-675 678 698 700 703 708 720 725-726 731 738-739 743-744 750-753 757 759 763-765 767 772-779 787 789-790 798 800 810 823 829 834-836 841 848 854-856 859 861 864 870-871 881 890-891 898 908-909 913 928 933 941 949 958 961 963 967 969 975 981 986 988-990 992 999 1007-1008 1014 1016 1039 1041 1073-1074 1079 1089 1097 1109 1114-1117 1122 1131 1140-1141 1144-1145 1163 1172 1175-1177 1186 1196 1198 1206 1211 1216 1220 1223 1227 1234-1243 1261-1262 1267 1271 1280-1281 1284 1290 1308 1317-1320 1322 1324-1325 1327 1330 1334-1335 1339 1346 1350-1351 1355 1357 1360 1370 1374 1377-1379 1386 1389-1390 1392 1397 1400 1402 1406-1407 1417 1423 1425-1427 1440-1441 1466 1474 1477 1483 1493 1498 1504 1506 1525 1536 1545 1549 1566 1594 1598-1600 1608 1611 1614 1621 1623 1625 1632 1639 1641 1644 1647 1649 1653-1656 1658 1662-1663 1671 1673 1678-1681 1686-1688 1693 1705 1707 1711 1717-1718 1726-1727 1731-1733 1737-1738 1743-1745 1750-1761 1771-1772 1779 1786

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
thyroid gland	Clontech	THR001	4 9-10 20-21 37-39 48 50-51 54-57 60-61 65-66 71 83 94-96 98-100 102 104 110 112 115-117 119 123 127 133 136-137 140 149 152-153 155-158 163-164 168-169 171 186 190-192 197 201-203 219-220 229 233-237 246-247 253 256 258 262 265-266 268-269 277 280-281 284-286 288-289 298-299 302 309-311 317 321 326 332 335 341-342 344 348 350 354 358-359 363 368 371-373 382-383 385 394 398 400-401 411 414-415 421 424 430-431 433-436 443-446 450-452 454-455 458 472-474 476-478 482 484-485 487-488 490-494 496-497 500-501 503-504 506 509-513 516-517 519 524 526-527 529 535-540 547 549 562 564 569-570 575-576 588 594-595 601-602 604 606 610 612 615-617 619-623 628-630 634-635 642 647 649-651 660 662-665 668 670 681 690-694 696 698 700 709 721 727-729 732 734 738 740-741 743 745 750 759 761 763 765 770 773 780 785 795-796 798 802 804 823-824 826 828 833 838 841-845 847 849 857-860 867 874-875 878 880-881 887-888 890-892 894-895 898 908 910-911 913-914 922-923 926-927 929 932-934 937 939 941-942 948 953 957 961 963-964 966 978-979 981-982 987 990 992 1001 1004-1006 1010 1014 1020 1024 1033 1038-1039 1044 1047 1050 1052-1054 1056 1058 1068 1070-1071 1077-1079 1088 1094-1097 1105-1106 1112-1113 1116-1117 1124 1126 1128-1129 1131 1134 1136-1137 1142-1143 1146-1147 1149-1150 1156 1161-1164 1167 1170-1173 1177-1181 1190 1192 1197 1200 1204 1208-1209 1214 1217 1219 1222 1230 1232-1233 1235 1241 1245 1247 1254 1257-1258 1260 1262 1271-1273 1283 1286-1289 1299 1306 1314 1320 1330-1332 1334-1335 1342 1345 1349 1365-1367 1370-1372 1374 1381 1394 1407 1419 1428 1436-1437 1440-1441 1443 1446-1449 1454 1459 1461-1462 1468 1470-1471 1475 1477 1479 1482 1491 1497-1498 1504-1505 1507 1513 1522 1524-1526 1528 1531 1534 1536-1537 1548 1550 1553 1555-1559 1562 1567 1570 1590-1591 1597 1599-1601 1612 1614 1616 1619-1620 1622 1624-1626 1628 1631-1632 1634 1636 1639 1644-1645 1648 1651 1653-1656 1658 1660 1662-1663 1667 1669 1671 1675 1678-1681 1683-1686 1689 1691-1692 1703 1709-1711 1717 1724-1726 1729 1734 1737-1738 1740 1743-1744 1749 1753 1759-1761 1770 1777 1786
trachea	Clontech	TRC001	9 29-31 46 48 87 104 107 110 135 158 222 262 266 286 301 318 331

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			352 372 377 384 414 424 445-446 454 472 474 491 496 560 579 588 593 597 607 612 626 681 702 719 810 859 866 878 894-895 912 916 922 932 935 1046 1075 1080 1099-1102 1113 1208 1215 1232-1233 1237 1281 1312 1385 1387 1405 1414 1424 1430 1437 1447 1505 1569 1579 1586 1600 1641 1653 1667 1671 1676-1677 1683 1691-1692 1711 1717 1726 1772
uterus	Clontech	UTR001	17 19 25 41 46 57-58 61 69 104 108 139 152 174 198 200-201 206 263-265 274 290 387 408 420 438 446 448 452 473 491 493 499 503 506 513 519 522 526 530 542-543 560 601 610 632 659 665 720 751 773 780 833 845 857 872 877 912 929 934 937 996 1009-1011 1018 1050 1075 1107 1124 1170 1219 1258 1279 1287 1310 1320 1323 1343-1344 1375 1437 1451-1452 1478 1481 1498 1519 1521 1536 1552 1579 1597 1602 1606 1620 1626-1627 1649 1652 1661 1670 1719 1722-1723

TRADOCS:1416191.1(%CQN011.DOC)

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	Y41736	Homo sapiens	Human PRO1114 protein sequence.	1398	100
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated-kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
5	X02761	Homo sapiens	fibronectin precursor	10535	98
6	X02761	Homo sapiens	fibronectin precursor	8990	89
8	X02761	Homo sapiens	fibronectin precursor	12564	99
9	AJ011679	Homo sapiens	Rab6 GTPase activating protein, GAPCenA	5251	99
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	11336	98
12	Z97630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein RIP60	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
19	U00059	Saccharomyces cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	2300	99
24	AJ289131	Homo sapiens	chondroitin 4-O-sulfotransferase	2211	99
25	U33460	Homo sapiens	DNA-directed RNA polymerase I, largest subunit	8777	98
26	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
27	U43701	Homo sapiens	ribosomal protein L23a	791	100
28	U02032	Homo sapiens	ribosomal protein L23a	767	97
29	Y41124	Homo sapiens	Human secreted protein encoded by gene 17 clone HNFIY77.	1083	99
30	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1811	100
33	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
35	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1667	99
36	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1104	98
37	Y78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	3586	78
38	Y78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	4726	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
39	Y78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	3556	77
40	U93121	Homo sapiens	M-phase phosphoprotein-1	3747	100
41	Y42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	795	100
42	AF282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	EIF-1	2724	88
45	U19617	Mus musculus	EIF-1	2062	86
46	AF100758	Homo sapiens	osteoinductive factor OIF	1538	100
47	Y87591	Homo sapiens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
49	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus norvegicus	rab-related GTP-binding protein	1089	96
53	L31783	Mus musculus	uridine kinase	917	71
54	X83973	Homo sapiens	transcription factor	4486	98
55	AF224741	Homo sapiens	chloride channel protein 7	4128	99
56	W74835	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	1491	100
57	Z50907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	Y66660	Homo sapiens	Membrane-bound protein PRO783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1300_1 clone secreted protein.	157	30
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	Z82059	Caenorhabditis elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPA1 protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	Y41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
78	AL136538	Schizosaccharomyces pombe	similarity to S. cerevisiae kti12 protein	210	31
79	AF129756	Homo sapiens	G4	1554	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
80	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))	2033	100
81	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))	1220	96
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens	R26984_1	2700	98
84	X73113	Homo sapiens	fast MyBP-C	5959	99
85	AF097330	Homo sapiens	H1 chloride channel; p64H1; CLIC4	1305	99
86	AB018423	Mus musculus	SH2 domain-containing protein	1360	78
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	99
88	AF196329	Homo sapiens	triggering receptor expressed on monocytes 1	1214	100
89	AB016879	Arabidopsis thaliana	contains similarity to pre-mRNA splicing factor-gene_id:MRB17.2	634	36
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864	Mus musculus	phtf protein	619	61
92	A61971	unidentified	MCSP	11676	99
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino acid sequence SEQ ID NO:86.	3890	100
94	Y87231	Homo sapiens	Human signal peptide containing protein HSPP-8 SEQ ID NO:8.	1031	100
95	AF227741	Rattus norvegicus	protein kinase WNK1	2428	95
96	AF227741	Rattus norvegicus	protein kinase WNK1	1961	94
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3423	100
99	AC005783	Homo sapiens	R33083_1	1974	99
100	Y95293	Homo sapiens	Human GEF containing NEK-like kinase substrate sQNK.	4092	99
101	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	1509	100
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa protein AUP1	2042	96
104	AB015982	Homo sapiens	serine/threonine kinase	4718	100
105	AF151074	Homo sapiens	HSPC240	831	64
106	M35522	Canis familiaris	GTP-binding protein (rab7)	354	50
107	R99800	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of nerve cells.	2337	93
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1290	93
109	AC005614	Homo sapiens	P23269_2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo sapiens	Human PRO274 protein sequence.	2285	100
113	W15506	Homo sapiens	Mitogen activating protein kinase BRK1.	1991	100
114	Y71071	Homo sapiens	Human membrane transport protein, MTRP-16.	1190	99
115	AL049548	Homo sapiens	dJ398G3.1 (ortholog of rat CPG2)	3497	99
116	AF189817	Mus musculus	ovectin-2	1124	90
117	W30891	Homo	Human cytostatin III protein.	715	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		sapiens			
118	AF116618	Homo sapiens	PRO1038	1469	100
119	Y08915	Homo sapiens	alpha 4 protein	1748	100
120	AF098070	Drosophila melanogaster	Lis1 homolog	192	39
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling.	2637	98
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania major	glycoprotein 96-92	172	27
126	U75467	Drosophila melanogaster	Atu	935	36
127	Z68220	Caenorhabditis elegans	Similarity to Human ADP/ATP carrier protein	438	43
128	AF095927	Rattus norvegicus	protein phosphatase 2C	1927	94
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillus sakei	ribokinase RbsK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	3230	100
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein encoded by gene 154 clone HE6FL03.	480	100
137	W78200	Homo sapiens	Human secreted protein encoded by gene 75 clone HHGAU81.	855	99
138	AL033520	Homo sapiens	dJ349A12.1 (similar to KIAA0701 protein)	424	39
139	AF020261	Santalum album	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
141	Y06435	Homo sapiens	Human protease HUPM-8.	936	100
142	Z68493	Caenorhabditis elegans	predicted using Genefinder	385	42
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like protein	596	65
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A human proliferation and apoptosis related protein.	480	100
146	AB004906	Ipomoea purpurea	transposase	146	20
147	AC007357	Arabidopsis thaliana	F3P19.18	647	31
148	W75155	Homo sapiens	Human secreted protein encoded by gene 41 clone HNTME13.	1494	98
149	AF056490	Homo sapiens	cAMP-specific phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue HHH-7.	785	99
151	U10397	Saccharomyces cerevisiae	Yhr148wp	515	53
152	X73478	Homo sapiens	phosphotyrosyl phosphatase activator	1719	99
153	AL049697	Homo sapiens	dJ382I10.5.1 (novel protein	2034	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			similar to arginyl-tRNA)		
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein encoded from gene 6.	1471	100
158	W77404	Homo sapiens	Secreted salivary polypeptide zsig32.	937	100
159	Y17248	Homo sapiens	Human protein kinase inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible protein, HIFI.	484	98
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1357	100
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ ID NO: 7713.	463	97
165	AJ250839	Homo sapiens	serine/threonine protein kinase	1442	71
166	L09649	Zymomonas mobilis	zm2	173	37
167	Y73337	Homo sapiens	HTRM clone 1944530 protein sequence.	1204	100
168	W88645	Homo sapiens	Secreted protein encoded by gene 112 clone HUKFC71.	1084	100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE000871	Methanobacterium thermoautotrophicum	conserved protein	166	27
171	Y27684	Homo sapiens	Human secreted protein encoded by gene No. 118.	821	100
172	AF226044	Homo sapiens	HSNPRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779	100
174	D43949	Homo sapiens	This gene is novel.	3202	100
175	Y07923	Homo sapiens	GTP-binding protein	1205	100
176	W90338	Homo sapiens	Human DP1 homologue protein.	966	100
177	Y41675	Homo sapiens	Human channel-related molecule HCRM-3.	1122	100
178	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
179	AF220492	Homo sapiens	krueppel-like zinc finger protein HZF2	4100	99
180	X03084	Homo sapiens	C1q B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	1389	58
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	82
187	W75058	Homo sapiens	Human secreted protein encoded by gene 2 clone HLDBG33.	1188	99
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	100
190	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
191	Y22203	Homo sapiens	Human calcium-binding phosphoprotein, CBPP-1, protein sequence.	1083	99
192	W63692	Homo sapiens	Human secreted protein 12.	1975	100
193	W87772	Homo sapiens	Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.	2605	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
194	AF084259	Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh173_7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein gene clone hm236_1.	1614	100
199	Y44277	Homo sapiens	Human nucleic acid methylase-2.	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	Y87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	C1q C chain	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccharomyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccharomyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
225	AB032401	Mus musculus	mmDj4	1761	92
226	AB032401	Mus musculus	mmDj4	1988	92
227	X83502	Saccharomyces cerevisiae	J1007	112	26
228	X83502	Saccharomyces cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO820.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin B1.	2218	99
234	Y53762	Homo sapiens	A GTP-binding polypeptide	1017	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			designated RAQ.		
235	Z50749	Homo sapiens	yeast sds22 homolog	1800	100
236	Z50749	Homo sapiens	yeast sds22 homolog	1754	98
237	AB026491	Homo sapiens	PICK1	2137	100
238	AJ270205	Entodinium caudatum	putative phosphatidylinositol-4-phosphate 5-kinase	114	37
239	AB030189	Mus musculus	contains transmembrane (TM) region and ATP binding region	710	93
240	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3785	99
241	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3436	99
242	AF155107	Homo sapiens	NY-REN-37 antigen	996	99
243	AF155107	Homo sapiens	NY-REN-37 antigen	1005	100
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein similar to yeast and bacterial cytosine deaminase)	763	99
245	U37026	Rattus norvegicus	sodium channel beta 2 subunit	162	30
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans P55A12.9 (Tr:P91086))	2391	98
247	U32274	Saccharomyces cerevisiae	Ydr386wp; CAI: 0.12	191	37
248	Y41719	Homo sapiens	Human PRO864 protein sequence.	1879	100
249	AB029434	Homo sapiens	ghrelin precursor	611	100
250	X97831	Rattus norvegicus	carnitine/acylcarnitine carrier protein	246	38
251	W80993	Homo sapiens	Human RIP-interacting factor RIF.	1724	100
252	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
253	W59878	Homo sapiens	Amino acid sequence of the cDNA clone AIP-2 (HEBGM49).	765	100
254	AL354533	Leishmania major	possible adenylate kinase	265	34
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	Y78113	Homo sapiens	Human cytokine signal regulator CKSR-1 SEQ ID NO:1.	2247	99
257	AL035539	Arabidopsis thaliana	putative amino acid transport protein	390	27
258	W74787	Homo sapiens	Human secreted protein encoded by gene 58 clone HHFWN61.	1171	100
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein similar to protein kinase C inhibitors)	974	100
260	AE000909	Methanobacterium thermoautotrophicum	serine/threonine protein kinase related protein	363	30
261	AL050131	Homo sapiens	hypothetical protein	626	100
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel protein similar to APOBEC1)	1072	100
265	AF205940	Homo sapiens	endomucin	1289	100
266	AL023583	Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1101G7.3 (novel protein kinase domains containing protein similar to phosphoprotein C8FW)	1888	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
268	AF161470	Homo sapiens	HSPC121	1884	98
269	AF161470	Homo sapiens	HSPC121	1232	96
270	X90763	Homo sapiens	HHa5 hair keratin type I intermediate filament	2190	99
271	AF207600	Homo sapiens	ethanolamine kinase	1952	100
272	M32334	Homo sapiens	intercellular adhesion molecule 2	1436	100
273	AF161403	Homo sapiens	HSPC134	663	61
274	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.	587	100
276	Y77576	Homo sapiens	Human cytoskeletal protein (HCYT) (clone 2195418).	762	100
277	AF077042	Homo sapiens	30S ribosomal protein S7 homolog	1269	100
278	Y94907	Homo sapiens	Human secreted protein clone ca106_19x protein sequence SEQ ID NO:20.	1619	98
279	Y68788	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-20.	2801	99
280	Z75134	Canis familiaris	rod transducin	1816	100
281	Z75134	Canis familiaris	rod transducin	1718	96
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens	DC1	1859	99
285	AF156102	Homo sapiens	ELL complex EAP30 subunit	1318	99
286	Y35897	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 146.	1250	99
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	Y66724	Homo sapiens	Membrane-bound protein PRO836.	2321	100
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein (isoform 1))	1738	100
294	Y73348	Homo sapiens	HTRM clone 839651 protein sequence.	1245	99
295	L11672	Homo sapiens	zinc finger protein	1694	44
296	AL035423	Homo sapiens	dJ20I3.1 (brain mitochondrial carrier protein-1 (BMCP1))	1024	79
297	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
298	AF161417	Homo sapiens	HSPC299	1147	85
299	AF159141	Homo sapiens	breast cancer metastasis-suppressor 1	1236	99
300	U26397	Rattus norvegicus	inositol polyphosphate 4-phosphatase	160	30
301	AF036145	Homo sapiens	meningioma-expressed antigen 5	3458	100
302	Z82022	Homo sapiens	GlcNac-1-P transferase	2067	99
303	AF269232	Mus musculus	butyrophilin-like protein BUTR-1	271	50
304	AJ222644	Arabidopsis thaliana	asparaginyl-tRNA synthetase	659	50
305	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	351	79
306	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	3056	100
308	Y44486	Homo sapiens	Human GPRW receptor polypeptide.	1721	100
309	AJ131891	Homo sapiens	DNA polymerase mu	2598	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
310	AF293335	Homo sapiens	p30 DBC	1248	92
311	AF176525	Mus musculus	F-box protein FBL12	1501	93
312	X57802	Homo sapiens	immunoglobulin lambda light chain	959	81
313	Z36715	Homo sapiens	Net	2048	98
314	AF161532	Homo sapiens	HSPC047	727	100
315	AF208068	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	Y66666	Homo sapiens	Membrane-bound protein PRO1013.	1166	100
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	2243	99
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66.	913	100
324	Y13381	Homo sapiens	Amino acid sequence of protein PRO271.	1976	100
325	Y94944	Homo sapiens	Human secreted protein clone bf157_16 protein sequence SEQ ID NO:94.	2305	98
326	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	6728	99
327	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
328	Z78013	Caenorhabditis elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	Z75330	Homo sapiens) >R65207 R65207 02-MAR-1995 27-AUG-1993 Human stromalin-1. [Homo sapiens	nuclear protein SA-1	6492	99
331	AL008583	Homo sapiens	dJ327J16.3 (supported by GENSCAN, FGENES and GENEWISE)	2133	99
332	Y36104	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 489.	310	41
333	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598	Mus musculus	p53-regulated DDA3	997	64
335	M99058	Eimeria maxima	em100 gene is homologous the Eimeria tenella gene et100	154	26
336	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
337	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	2602	94
338	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3447	98
339	Z66561	Caenorhabditis elegans	Similarity to Human rab13 protein (PIR Acc. No. A49647).	716	34
340	AB021643	Homo sapiens	gonadotropin inducible transcription repressor-3	2761	99
341	G01946	Homo sapiens	Human secreted protein, SEQ ID NO: 6027.	465	98
342	AF020591	Homo sapiens	zinc finger protein	1091	48
343	L29154	Homo sapiens	immunoglobulin heavy chain	439	84

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			VDJ region		
344	U10281	Sus scrofa	gastric mucin	279	24
345	AK000404	Homo sapiens	unnamed protein product	1177	99
346	L22557	Rattus norvegicus	calmodulin-binding protein	1949	84
347	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
355	AJ010014	Homo sapiens	M96A protein	1269	47
356	AF151029	Homo sapiens	HSPC195	941	91
357	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
358	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	530	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	Homo sapiens	proSAAS	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366	U73200	Mus musculus	p116Rip	884	82
367	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabditis elegans	similar to the protein phosphates 2c family	549	36
370	Y73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371	AF272833	Homo sapiens	misato	2869	97
372	AF198454	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
373	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	273	80
374	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA.	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by genp 100 clone HLQAB52.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PRO0518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PRO703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AP-1 specific protein phosphatase	7008	98
383	U64608	Caenorhabditis elegans	coded for by C. elegans cDNA yk173c12.5	246	36
384	U50133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription factor-like nuclear regulator	4123	97

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
387	AF208845	Homo sapiens	BM-003	1375	99
389	X57821	Homo sapiens	immunoglobulin lambda light chain	797	76
390	AF182404	Homo sapiens	mitochondrial uncoupling protein 1	1670	99
391	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
393	AF178432	Homo sapiens	SH3 protein	3700	100
394	AF229928	Drosophila melanogaster	cytoplasmic protein 89BC	1616	62
395	AF181721	Homo sapiens	RU2S	2254	100
396	Y69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398	AL390137	Homo sapiens	hypothetical protein	263	51
399	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccharomyces pombe	WD repeat protein	447	27
401	AC004959	Homo sapiens	similar to 2-oxoglutarate dehydrogenase ; similar to Q02218 (PID:g152618)	4176	78
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to D.melanogaster CG5986 protein)	761	100
404	Z60753	Caenorhabditis elegans	ZC518.3b	888	48
405	Z78013	Caenorhabditis elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
406	AB031230	Homo sapiens	protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein HTMPN-69.	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310O13.7 (novel protein similar to H. roretzi HRPET-3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing subunit	2961	99
416	U43503	Saccharomyces cerevisiae	Lphip	115	42
417	AL160493	Leishmania major	possible t26f17.21	239	35
418	Y08100	Homo sapiens	Human PRO331 protein.	330	29
419	U15131	Homo sapiens	p126	2228	54
420	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
421	AF190835	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate-binding protein-2	1962	100
423	AL137530	Homo sapiens	hypothetical protein	433	94
424	X63753	Homo sapiens	con-a	7269	100
425	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
426	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1084	55

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
427	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1259	56
428	AE003683	Drosophila melanogaster	CG8312 gene product	149	29
429	Y07829	Homo sapiens	RING finger protein	2201	99
430	AF096897	Drosophila melanogaster	pushover	4442	47
431	U41387	Homo sapiens	Gu protein	4021	99
432	AF023674	Homo sapiens	nephrocystin	3783	100
433	AF146760	Homo sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis thaliana	cleft lip and palate associated transmembrane protein-like	886	42
437	Y94247	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase	1075	63
439	AF105228	Bos taurus	tuftelin	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-577)	4897	98
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1-938)	3979	81
443	Y66689	Homo sapiens	Membrane-bound protein PRO1136.	3299	99
444	AC067754	Arabidopsis thaliana	unknown protein; 20348-23707	114	33
445	AF229032	Mus musculus	piL	2077	93
446	AF056035	Rattus norvegicus	s-nexilin	2662	85
447	AF132484	Mus musculus	unknown	478	51
448	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	528	45
449	AF161445	Homo sapiens	HSPC327	1606	100
450	Z68753	Caenorhabditis elegans	ZC518.3b	951	49
451	W39160	Homo sapiens	Human partial complement factor H protein fragment 3.	155	32
452	W85727	Homo sapiens	Novel protein (Clone BM46_10).	2799	99
453	Y53629	Homo sapiens	A bone marrow secreted protein designated BMS115.	2810	100
454	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	4069	100
455	AF240468	Homo sapiens	nicastrin	3687	100
456	Z15005	Homo sapiens	CENP-E	13305	99
457	M59216	Homo sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	Y73467	Homo sapiens	Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.	966	100
459	W67824	Homo sapiens	Human secreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	279	19
461	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	9196	99
462	G04044	Homo sapiens	Human secreted protein, SEQ ID NO: 8125.	486	93
463	AC002398	Homo sapiens	P25965_1	1018	100
464	AF064856	Rattus sp.	7acomp protein	1845	84
465	AF223408	Homo sapiens	B99	3686	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
466	AF223408	Homo sapiens	B99	2878	87
467	AF104415	Mus musculus	gene trap locus-13	6336	91
468	U53450	Rattus norvegicus	Jun dimerization protein 1 JDP-1	196	49
469	AL031297	Homo sapiens	dJ97P20.1 (novel gene)	3564	99
470	AF257077	Homo sapiens	eukaryotic translation initiation factor EIF2B subunit 3	1274	95
471	L26125	Podospora anserina	beta transducin-like protein	284	38
472	Y84903	Homo sapiens	A human proliferation and apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	252	44
474	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	838	100
475	Y95006	Homo sapiens	Human secreted protein vel3_1, SEQ ID NO:52.	3411	100
476	D38549	Homo sapiens	hm1025 is new	6533	99
477	AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
478	AL031534	Schizosaccharomyces pombe	putative asparagine synthase	482	40
479	L28125	Podospora anserina	beta transducin-like protein	233	26
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens	centaurin beta2	3986	99
482	Z38061	Saccharomyces cerevisiae	mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	295	23
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
486	X57527	Homo sapiens	alpha 1(VIII) collagen	4166	99
487	Y19062	Homo sapiens	39k3 protein	2475	100
488	Y73373	Homo sapiens	HTRM clone 921803 protein sequence.	555	56
489	AL021910	Homo sapiens	D34I8.1 (Kruppel related Zinc Finger protein 184)	4184	100
490	X53773	Rattus norvegicus	alpha-c large chain (AA 1-938)	4675	97
491	U52426	Homo sapiens	GOK	1459	59
492	AL359773	Leishmania major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportin1	2929	100
494	Z93241	Homo sapiens	dJ222E13.1 (novel protein with some similarity to Drosophila KRAKEN)	513	96
495	AF036377	Homo sapiens	unknown	1812	100
496	U93564	Homo sapiens	p40	133	45
497	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	357	100
498	AF069781	Drosophila melanogaster	Bem46-like protein	653	43
499	Y16601	Homo sapiens	Human cell-cycle phosphoprotein CECYP-2.	1658	98
500	X70944	Homo sapiens	PTB-associated splicing factor	3883	100
501	AF027503	Mus musculus	putative membrane-associated guanylate kinase 1	205	36
502	AF282874	Homo sapiens	nectin 3; PRR3	2856	99
503	AJ249732	Homo sapiens	G8 protein	669	100
504	AF208861	Homo sapiens	BM-019	1629	100
505	L09708	Homo sapiens	complement component C2	4022	100
507	X66285	Mus musculus	HC1 ORF	115	43
508	D00189	Rattus norvegicus	Na+,K+-ATPase alpha-subunit	5227	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
509	Y94971	Homo sapiens	Human secreted protein clone fa171_1 protein sequence SEQ ID NO:140.	2176	100
510	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	781	77
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
513	X84908	Homo sapiens	phosphorylase kinase	5729	99
514	X52851	Homo sapiens	peptidylprolyl isomerase	650	76
515	AF186084	Homo sapiens	epidermal growth factor repeat containing protein	3046	99
516	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	505	99
517	U04706	Bos taurus	50 kDa protein	1749	77
518	G00653	Homo sapiens	Human secreted protein, SEQ ID NO: 4734.	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobus fulgidus	chromosome segregation protein (smc1)	153	20
523	AF062249	Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	83
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting protein	524	79
528	D49387	Homo sapiens	NADP dependent leukotriene b4 12-hydroxydehydrogenase	1616	100
529	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKFZP564A032, SBBI88) similar to mouse IFN-gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabditis elegans	carrier protein (c2)	576	50
533	X76116	Caenorhabditis elegans	carrier protein (c2)	506	50
534	X12966	Homo sapiens	3-oxoacyl-CoA thiolase propeptide (424 AA)	1972	100
535	Y09267	Homo sapiens	flavin-containing monooxygenase 2	2486	100
536	Z11773	Homo sapiens	SRE-ZBP	2201	99
537	D84224	Homo sapiens	methionyl tRNA synthetase	4741	99
538	D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
539	D84224	Homo sapiens	methionyl tRNA synthetase	2933	96
540	D84224	Homo sapiens	methionyl tRNA synthetase	4529	99
541	J03244	Bos taurus	H+ ATPase 31kDa subunit (EC 3.6.1.3)	848	77
542	Y92514	Homo sapiens	Human OXRE-11.	2301	99
543	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	2151	61
544	AE000919	Methanobacterium thermoautotrophicum	conserved protein	207	38
545	A06669	synthetic construct	preTGF-beta1	2070	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
546	Y02698	Homo sapiens	Human secreted protein encoded by gene 49 clone HTPCS60.	854	98
547	AP112205	Homo sapiens	WSB-1 protein	2275	100
548	X60271	Mus musculus	c-rel	2264	74
549	AC016827	Arabidopsis thaliana	putative GTPase	810	42
550	Y70400	Homo sapiens	Human cell-signalling protein-2.	429	68
551	AB048365	Homo sapiens	NEDD4-like ubiquitin ligase 1	8290	99
552	Y57880	Homo sapiens	Human transmembrane protein HTMPN-4.	1112	95
553	AP119855	Homo sapiens	PRO1847	265	67
554	M17236	Homo sapiens	MHC HLA-DQ alpha precursor	1332	100
555	AL078468	Arabidopsis thaliana	putative protein	540	40
556	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	515	44
557	AK024487	Homo sapiens	FLJ00086 protein	1623	98
558	M12140	Homo sapiens	pol gene protein; Xxx	117	48
559	W74825	Homo sapiens	Human secreted protein encoded by gene 97 clone HAQBF73.	225	56
560	X56681	Homo sapiens	junD protein	373	88
561	AF003136	Caenorhabditis elegans	contains weak similarity to an AMP-binding motif	2926	54
562	AL109839	Homo sapiens	dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
563	AF181640	Drosophila melanogaster	BcDNA.GH09817	289	42
564	AF052723	Feline leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
565	AF161472	Homo sapiens	HSPC123	439	44
566	Y28817	Homo sapiens	pt326_4 secreted protein.	3338	100
567	U09848	Homo sapiens	zinc finger protein	1738	100
569	AF155113	Homo sapiens	NY-REN-55 antigen	3603	93
570	AF155113	Homo sapiens	NY-REN-55 antigen	3951	99
571	AL032821	Homo sapiens	dJ55C23.1 (vanin 1)	1821	98
572	M69181	Homo sapiens	non-muscle myosin B	7350	99
573	M69181	Homo sapiens	non-muscle myosin B	7311	98
574	Y59679	Homo sapiens	Secreted protein 108-008-5-0-E6-PL.	772	100
575	AL365234	Arabidopsis thaliana	putative protein	788	40
576	AL365234	Arabidopsis thaliana	putative protein	788	40
577	X06745	Homo sapiens	DNA polymerase alpha-subunit (AA 1 - 1462)	7619	99
578	AB041642	Homo sapiens	PAR-6	1342	100
579	D86984	Homo sapiens	similar to yeast adenylate cyclase (SS6776)	2446	100
580	AP165124	Homo sapiens	gamma-aminobutyric acid A receptor gamma 2	2499	99
581	W88812	Homo sapiens	Polypeptide fragment encoded by gene 58.	2339	99
582	U82319	Homo sapiens	novel ORF	342	100
583	P92219	Homo sapiens (human)	CR1 protein.	11425	99
584	AJ223948	Homo sapiens	RNA helicase	6608	99
585	Y08612	Homo sapiens	88kDa nuclear pore complex protein	3874	99
586	Y42384	Homo sapiens	Amino acid sequence of lv310_7.	1007	37
587	AF129756	Homo sapiens	BAT4	1873	98

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
588	AP131775	Homo sapiens	Unknown	1929	99
589	AJ250865	Homo sapiens	TBSS 2	2348	100
591	Z98885	Homo sapiens	dJ522J7.2 (bromodomain-containing 1 (similar to peregrin, BR140))	4167	100
592	L76571	Homo sapiens	nuclear hormone receptor	1355	100
593	AF091622	Homo sapiens	PHD finger protein 3	9054	100
594	X56807	Homo sapiens	desmocollin type 2a	4443	100
595	AL137802	Homo sapiens	dJ758A10.1 (novel protein)	212	55
596	AL022329	Homo sapiens	bK407F11.2 (adrenergic, beta, receptor kinase 2)	3653	100
597	AF226048	Homo sapiens	GL003	2009	99
598	AJ278112	Homo sapiens) >Y49635 Y49635 21-OCT-1999 15-APR-1998 Human sdp3.5 protein. [Homo sapiens	putative cell cycle control protein	335	23
599	Y59741	Homo sapiens	Human normal ovarian tissue derived protein 18.	1574	99
600	L36531	Homo sapiens	integrin alpha 8 subunit	5386	99
601	Y38458	Homo sapiens	Human secreted protein encoded by gene No. 20.	895	100
602	AF218584	Homo sapiens	GGA1	3365	100
603	Y13115	Homo sapiens	serine/threonine protein kinase	5071	99
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
606	Y14494	Homo sapiens	aralar1	3465	99
607	AJ001981	Homo sapiens	OXA1L	2603	100
608	X86098	Homo sapiens	binds directly to adenovirus type 5 E1A protein	3069	100
610	AF163572	Homo sapiens	Forssman glycolipid synthetase	1865	99
611	AF161503	Homo sapiens	HSPC154	1261	97
612	L41834	Ensis minor	nuclear protein	345	30
613	Y91954	Homo sapiens	Human cytoskeleton associated protein 9 (CYSKP-9).	3668	100
614	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	361	94
615	X85786	Homo sapiens	binding regulatory factor	3203	100
616	Y08319	Homo sapiens	kinesin-2	3487	99
617	D12644	Mus musculus	KIF2 protein	3609	97
618	U28789	Mus musculus	PACT	5936	89
619	Y35914	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 163.	1684	99
620	AB046382	Mus musculus	testis-abundant finger protein	199	23
621	Y00062	Homo sapiens	precursor polypeptide (AA -23 to 1120)	3440	99
622	AF068286	Homo sapiens	HDCMD38P	861	100
623	X98248	Homo sapiens	sortilin	4436	99
624	X61100	Homo sapiens	75 kDa subunit NADH dehydrogenase precursor	3734	99
625	S58544	Homo sapiens	75 kda infertility-related sperm protein	2125	99
626	AF151027	Homo sapiens	HSPC193	582	93
627	X14968	Homo sapiens	RII-alpha subunit (AA 1-404)	2079	100
628	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein	1983	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
629	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein	1694	100
630	AF098786	Homo sapiens	17 beta-hydroxysteroid dehydrogenase type VII	1754	100
631	AL034555	Homo sapiens	dJ134O19.3 (zinc finger protein 151 (pHZ-67))	4273	100
632	W74826	Homo sapiens	Human secreted protein encoded by gene 98 clone HAQBT94.	794	96
633	AF288288	Homo sapiens	HPT protein	2236	100
634	AF041429	Homo sapiens	pRGR1	823	99
635	X66357	Homo sapiens	serine/threonine protein kinase	1589	100
636	Y11284	Homo sapiens	AFX1	2571	98
637	AB004884	Homo sapiens	PKU-alpha	3718	99
638	AJ002303	Homo sapiens	synaptogyrin 1c	1020	100
639	AJ002304	Homo sapiens	synaptogyrin 1b	1002	100
640	AJ002303	Homo sapiens	synaptogyrin 1c	933	94
641	D87682	Homo sapiens	similar to a C.elegans protein encoded in cosmid T26A5.	2676	100
642	M14660	Homo sapiens	ISG-K54	2473	99
643	X06661	Homo sapiens	calbindin (AA 1-261)	1358	100
644	AF119900	Homo sapiens	PRO2822	185	76
645	AB031048	Drosophila melanogaster	microtubule associated-protein orbit	738	27
646	AF250842	Drosophila melanogaster	multiple asters	834	29
647	X86691	Homo sapiens	MI-2 protein	10110	99
648	U67934	Homo sapiens	44.9 kDa protein C18B11 homolog	827	96
649	AF236061	Oryctolagus cuniculus	RING-finger binding protein	3830	91
650	AL034553	Homo sapiens	dJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))	5708	100
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2388	99
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	Y57908	Homo sapiens	Human transmembrane protein HTMPN-32.	608	99
656	Z34975	Homo sapiens	IdICp	3733	100
658	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
659	W76734	Homo sapiens	Human mDia Rho targeting protein.	781	34
660	AF202724	Homo sapiens	Sad1 unc-84 domain protein 1	2172	100
661	Z21966	Homo sapiens	mPOU homeobox protein	1529	100
662	AJ242954	Mus musculus	dysferlin	4752	59
663	AF182316	Homo sapiens	myoferlin	6232	99
665	AL161516	Arabidopsis thaliana	hypothetical protein	209	30
667	X59303	Homo sapiens	valyl-tRNA synthetase	3393	99
668	Y13355	Homo sapiens	Amino acid sequence of protein PRO220.	3692	100
669	AB010692	Arabidopsis thaliana	contains similarity to endo-beta-N-acetylglucosaminidase gene	611	52
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter 3	2902	99
673	AF269223	Homo sapiens	TCP11	806	42
674	AF229633	Mus musculus	groucho-related protein 4	4053	99
675	L14463	Rattus norvegicus	transducin	3619	92

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
676	AC005757	Homo sapiens	R32611_1	2779	100
677	S61069	Homo sapiens	reverse transcriptase homolog=pol (retroviral element)	252	65
678	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
679	X79066	Homo sapiens	ERF-1	1783	100
680	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKa83 protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99
684	Y94952	Homo sapiens	Human secreted protein clone fh116_11 protein sequence SEQ ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257I20.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia coli	orf, hypothetical protein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
688	AF039697	Homo sapiens	antigen NY-CO-31	508	98
689	U09355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	Dlx-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693	X90530	Homo sapiens	ragB	1405	99
694	X90530	Homo sapiens	ragB	1590	85
695	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase	669	52
697	AJ250425	Rattus norvegicus	Collybistin I	2455	98
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184	99
703	AJ243274	Homo sapiens	AP-2rep protein	2078	99
704	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1697	94
705	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1736	99
706	Y41257	Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
707	AL022237	Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
710	Y08698	Homo sapiens	ranbp3	2849	98
711	Y68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.	754	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
712	U93574	Homo sapiens	putative p150	799	59
713	AC004531	Homo sapiens	Gene with similaity to DEAD box helicases	2715	99
714	D89016	Homo sapiens	Neuroblastoma	538	48
715	Y92175	Homo sapiens	Human cardiovascular system associated protein tyrosine phosphatase 2.	734	98
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil phosphoribosyltranferase)	862	100
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GQ1b alpha synthase	1696	93
718	Y96290	Homo >P40254 P40254 25-OCT-1984 09-APR-1983 Human IgD. [Homo sapiens	Human IGFAM-2 immunoglobulin.	2345	85
719	X07979	Homo sapiens	integrin beta 1 subunit precursor	4347	99
720	AJ224819	Homo sapiens	tumor suppressor	2149	99
721	Y07595	Homo sapiens	transcription factor TFIIH	2373	100
722	W41565	Homo sapiens) >W41564 W41564 08-OCT-1997 05-APR-1996 Human calpain. [Homo sapiens	Human calpain.	1591	99
723	AP161341	Homo sapiens	HSPC078	1097	98
724	AP187318	Homo sapiens	F-box protein Fbx2	1607	100
725	AC006708	Caencrhabdit is elegans	contains simlarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876)	1143	46
726	AC006708	Caenorhabdit is elegans	contains simlarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876)	988	46
727	AC024818	Caenorhabdit is elegans	contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	950	44
728	AJ005897	Homo sapiens	JM5	831	47
729	Y45377	Homo sapiens	Human secreted protein fragment encoded from gene 27.	908	97
730	G03931	Homo sapiens	Human secreted protein, SEQ ID NO: 8012.	578	100
731	AB012720	Oncorhynchus masou	GTP-binding protein	3865	76
732	W73404	Homo sapiens	Human secreted protein encoded by Gene No. 8.	862	97
733	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
734	AC024813	Caenorhabdit is elegans	Hypothetical protein Y54F10AL.a	152	24
735	AL035461	Homo sapiens	dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	1562	98
736	U00033	Caenorhabdit is elegans	similar to S. cerevisiae YJU2 protein	605	41
737	AF079098	Homo sapiens	arginine-tRNA-protein transferase 1-1p; ATE1-1p	2733	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	2793	100
739	AJ133115	Homo sapiens	TSC-22-like protein	2054	99
740	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
741	X98258	Homo sapiens	M-phase phosphoprotein 9	564	74
742	U97191	Caenorhabdit is elegans	strong similarity to the YPT1 sub-family of RAS proteins	960	85
743	X76057	Homo sapiens	phosphomannose isomerase	2191	100
744	G03209	Homo sapiens	Human secreted protein, SEQ ID NO: 7290.	496	98
745	X97064	Homo sapiens	Sec23 protein	4034	99
746	W93946	Homo sapiens	Human regulatory molecule HRM-2 protein.	994	100
747	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	1565	99
748	M19529	Sus scrofa	folliistatin A	1906	98
749	AJ249457	Trichomonas vaginalis	centrin, putative	183	20
750	AC004410	Homo sapiens	fos39554_1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity factor Sp1	4005	100
753	AB049629	Homo sapiens	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	1375	99
754	D79205	Homo sapiens	ribosomal protein L39	160	77
755	AB008430	Homo sapiens	CDEP	142	29
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	54
760	Y44250	Homo sapiens	Human cell signalling protein-13.	625	100
761	AF218586	Homo sapiens	Cide-b	1136	100
762	U38934	Gallus gallus	histone H2A	625	97
763	AF226053	Homo sapiens	HSKM-B	606	32
764	X13403	Homo sapiens	Oct-1 protein (AA 1 - 743)	3626	100
765	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	568	38
766	AL023828	Caenorhabdit is elegans	Y17G7B.14	200	27
767	Y82777	Homo sapiens	Human chordin related protein (Clone dw665_4).	2551	99
768	X92475	Homo sapiens	ITBA1	1429	100
769	Y42752	Homo sapiens	Human calcium binding protein 3 (CaBP-3).	1426	100
770	X51416	Homo sapiens	hormone receptor hERR1 (AA 1-521)	2641	97
771	AJ006591	Homo sapiens	cysteine-rich protein	1793	100
772	A08695	Homo sapiens	rap2	935	100
773	Z12173	Homo sapiens	N-acetylglucosamine-6-sulphatase	2970	100
774	Y91950	Homo sapiens	Human cytoskeleton associated protein 5 (CYSKP-5).	565	43
776	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
777	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
778	G01880	Homo sapiens	Human secreted protein, SEQ ID NO: 5961.	849	98
779	AJ012590	Homo sapiens	glucose 1-dehydrogenase	4185	99
780	AL078582	Homo sapiens	dJ1130E4.2 (KIAA0796)	1321	68
781	Z75955	Caenorhabdit is elegans	similar to mitochondrial carrier protein	384	34
782	AL109965	Homo sapiens	dJ1121G12.2 (SCAN domain-containing 1 protein)	900	100
783	AF061262	Mus musculus	semaF cytoplasmic domain associated protein 2	1316	83
784	G03873	Homo sapiens	Human secreted protein, SEQ	649	95

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 7954.		
785	Y84441	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2074	100
786	Y00918	Homo sapiens	Human Rab protein, RABP-1, protein sequence.	1048	99
787	Z97029	Homo sapiens	ribonuclease HI large subunit	1548	99
788	AB035384	Homo sapiens	SRp25 nuclear protein	962	94
789	AF024631	Homo sapiens	ANG2	2644	100
790	AJ006710	Rattus norvegicus	phosphatidylinositol 3-kinase	4508	97
792	V00638	bacteriophage lambda	reading frame ea10	600	100
793	AF049103	Homo sapiens	Huntingtin interacting protein	819	100
795	Z26317	Homo sapiens	desmoglein 2	4810	99
796	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	5080	99
797	U15155	Gallus gallus	trypsinogen	372	37
798	U97189	Caenorhabditis elegans	strong similarity to thw P13/P14 family of kinases	227	28
799	AF112201	Homo sapiens	neuronal protein NP25	1053	100
800	AF234765	Rattus norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	958	63
801	AF267852	Homo sapiens	placental protein 13-like protein	743	99
802	AF208851	Homo sapiens	BM-009	766	80
803	Z81097	Caenorhabditis elegans	Similarity to Human retinoblastoma-binding protein RBAP46 yk662d12.5 comes from this gene	152	27
804	G02113	Homo sapiens	Human secreted protein, SEQ ID NO: 6194.	496	98
805	AL121673	Homo sapiens	DA305P22.1 (novel protein)	1160	100
806	AC013483	Arabidopsis thaliana	putative GTPase activator protein	264	30
807	AC013483	Arabidopsis thaliana	putative GTPase activator protein	264	30
808	AB013885	Homo sapiens	beta-ureidopropionase	1494	100
809	AF078842	Homo sapiens	HOTTL protein	1581	99
810	AF161421	Homo sapiens	HSPC303	2134	96
811	AF261689	Homo sapiens	DNA polymerase epsilon p17 subunit	734	100
812	Z74029	Caenorhabditis elegans	Similarity to C.elegans alcohol dehydrogenase comes from this gene	610	71
813	Z73497	Homo sapiens	cU240C2.2 (Core histone H2A/H2B/H3/H4)	324	100
814	W87689	Homo sapiens	Human HTXFT19 polypeptide.	1484	99
815	X16282	Homo sapiens	zinc finger protein (217 AA) (1 is 2nd base in codon)	1109	99
816	Z92539	Mycobacterium tuberculosis	pth	300	36
818	AB030483	Mus musculus	B9	197	27
819	AL117555	Homo sapiens	hypothetical protein	321	94
820	AC005328	Homo sapiens	R26660_2, partial CDS	865	97
821	G03951	Homo sapiens	Human secreted protein, SEQ ID NO: 8032.	700	99
822	L34807	Musca domestica	transposase	174	20
823	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7009.	558	78
824	Z99531	Schizosaccha	caffeine-induced death	184	29

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		romyces pombe	protein 1		
825	AJ006692	Homo sapiens	ultra high sulfer keratin	693	68
826	U23037	Oryctolagus cuniculus	eIF-2Bepsilon	3406	90
827	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
828	Y30827	Homo sapiens	Human secreted protein encoded from gene 17.	113	44
829	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
830	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
832	AB011542	Homo sapiens	MEGF9	2097	100
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	223	70
834	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1574	100
835	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1144	89
836	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1448	94
837	X12517	Homo sapiens	C protein (AA 1-159)	918	100
838	U32865	Drosophila melanogaster	linotte protein	164	24
839	AF067730	Homo sapiens	TLS-associated protein TASR-2	631	56
840	U27831	Homo sapiens	striatum-enriched phosphatase	2840	98
841	AF286366	Homo sapiens	CamKY-like protein kinase	1796	100
842	G02309	Homo sapiens	Human secreted protein, SEQ ID NO: 6390.	278	98
843	AE003615	Drosophila melanogaster	adeJ gene product	113	48
844	G01350	Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	629	100
845	U27839	Mus musculus	glycosyl-phosphatidyl-inositol-anchored protein homolog	3305	96
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Dif33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1548	100
852	Z22968	Homo sapiens	M130 antigen	6208	100
853	Z22971	Homo sapiens	M130 antigen extracellular variant	6380	100
854	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	330	96
855	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	203	100
856	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis thaliana	putative cleavage and polyadenylation specifity factor	1383	55
858	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
859	L02956	Xenopus laevis	ribonucleoprotein	1664	85
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus	uridine kinase	1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabditis elegans	mitochondrial carrier protein	370	43
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			receptor associated protein		
865	AE001530	Helicobacter pylori J99	putative	230	32
866	X57807	Homo sapiens	immunoglobulin lambda light chain	699	91
867	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 10 C2H2 type Zinc finger domains)	4066	99
868	Y11652	Homo sapiens	phosphate cyclase	238	100
869	AF192968	Homo sapiens	high-glucose-regulated protein 8	3041	99
870	AB020648	Homo sapiens	KIAA0841 protein	3237	99
871	AL031427	Homo sapiens	dJ167A19.1 (novel protein)	1608	100
872	AF151534	Homo sapiens	core histone macroH2A2.2	1866	100
873	AL021331	Homo sapiens	dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein)	1129	100
874	X14608	Homo sapiens	propionyl-CoA carboxylase	3579	100
875	AL117334	Homo sapiens	dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249))	306	100
876	X79489	Saccharomyces cerevisiae	E-925 protein	446	35
877	Y53001	Homo sapiens	Human secreted protein clone dn834_1 protein sequence SEQ ID NO:8.	811	100
878	AF281064	Homo sapiens	CHMP1.5	957	100
879	X79417	Sus scrofa	40S ribosomal protein S12	687	100
880	AF001317	Saccharomyces cerevisiae	Soi1p	478	28
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEQ ID NO:52.	2547	100
882	M14036	Homo sapiens	C1-inhibitor	598	77
883	AB041261	Homo sapiens	calcium-independent phospholipase A2	2903	100
884	AF020313	Mus musculus	proline-rich protein 48	999	84
885	Y10936	Homo sapiens	hypothetical protein	1104	99
886	AF073997	Mus musculus	myotubularin related protein 1	866	36
887	Y57893	Homo sapiens	Human transmembrane protein HTMPN-17.	1099	94
888	AL117635	Homo sapiens	hypothetical protein	929	99
889	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2046	99
890	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	583	100
891	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	192	57
892	AF237631	Homo sapiens	ubiquitous tropomodulin U-Tmod	1798	100
893	AF090929	Homo sapiens	PRO0477p	653	99
894	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YRR082C, M. sexta MNG10 and C. elegans F28D1.1)	3196	100
895	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	2825	96
896	AF171102	Homo sapiens	retinal degeneration B beta	1302	95
897	AE003551	Drosophila melanogaster	CG18176 gene product	633	33

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
898	AJ237946	Homo sapiens	DEAD Box Protein 5	2443	100
899	Z97184	Homo sapiens	HKE2	624	100
900	Z97184	Homo sapiens	HKE2	409	98
901	AJ245587	Homo sapiens	Kruppel-type zinc finger	1942	100
902	AF091034	Homo sapiens	GTP-binding protein RAB22A	1011	100
903	R95953	Homo sapiens	Eukaryotic cell growth inhibiting factor.	414	96
904	L04733	Homo sapiens	kinesin light chain	1936	72
905	AE003540	Drosophila melanogaster	CG10984 gene product	446	33
906	M55542	Homo sapiens	guanylate binding protein isoform I	2993	98
907	M55542	Homo sapiens	guanylate binding protein isoform I	2901	96
908	W84085	Homo sapiens	Human membrane fusion protein WDProt.	1889	100
909	AF168676	Homo sapiens	TNF intracellular domain-interacting protein	647	100
910	AB029150	Homo sapiens	KRAB zinc finger protein HPB101L	2196	100
911	G02871	Homo sapiens	Human secreted protein, SEQ ID NO: 6952.	521	100
912	G03162	Homo sapiens	Human secreted protein, SEQ ID NO: 7243.	387	87
913	AJ243721	Homo sapiens] >Y92508 Y92508 13-APR-2000 06-OCT-1998 Human OXRE-5. [Homo sapiens	dTDP-4-keto-6-deoxy-D-glucose 4-reductase	1710	100
914	U24189	Caenorhabditis elegans	hypothetical protein 1207-1; Method: conceptual translation supplied by authors	244	41
915	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	843	99
916	AE000984	Archaeoglobus fulgidus	dinitrogenase reductase activating glycohydrolase (draG)	171	26
918	M23159	Cricetus cricetus	DHFR-comamplified protein	163	30
919	L12018	Caenorhabditis elegans	putative	1232	41
920	AF102177	Homo sapiens	tumor antigen SLP-8p	1260	97
921	AL096712	Homo sapiens	dJ744I24.2 (similar to a novel human gene mapping to Activator)	1017	78
922	AL161495	Arabidopsis thaliana	putative WD-repeat protein	866	42
923	AL161495	Arabidopsis thaliana	putative WD-repeat protein	442	36
924	U97001	Caenorhabditis elegans	similar to Schizosaccharomyces pombe	605	51
925	X71978	Mus musculus	Pif	1503	95
926	M92288	Drosophila melanogaster	beta-spectrin	290	51
927	Y27575	Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
928	Y22499	Homo sapiens	Human secreted protein sequence clone mh703_1.	2249	100
930	AJ224326	Homo sapiens	ribulose-5-phosphate-epimerase	912	100
931	U28991	Caenorhabdit	coded for by C. elegans cDNA	660	55

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		is elegans	cm21c7		
932	AL080065	Homo sapiens	hypothetical protein	210	25
933	G01884	Homo sapiens	Human secreted protein, SEQ ID NO: 5965.	767	98
934	AJ276485	Homo sapiens	integral membrane transporter protein	1200	100
935	AL035681	Homo sapiens	dJ756G23.3 (novel protein similar to drosophila transcriptional repressor)	1142	80
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB015345	Homo sapiens	HRIHFB2216	2601	99
938	X65724	Homo sapiens	ORF2	498	100
939	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	1487	100
940	G04047	Homo sapiens	Human secreted protein, SEQ ID NO: 8128.	117	100
941	AF094503	Homo sapiens	putative HIV-1 infection related protein	452	100
942	AC024200	Caenorhabditis elegans	contains similarity to several zinc finger proteins but not to the zinc finger domains	350	69
943	AF129756	Homo sapiens	G5c	273	100
944	M23765	Rattus norvegicus	alpha-tropomyosin	133	96
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	47
946	AF223468	Homo sapiens	AD021 protein	551	44
947	AF055473	Homo sapiens	GAGE-8	273	51
948	X75756	Homo sapiens	protein kinase C mu	2019	68
949	AF143956	Mus musculus	coronin-2	2300	93
950	Y36729	Homo sapiens	Human PGI protein sequence.	1861	99
951	W49041	Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis thaliana	gene_id:MXC17.7-	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL-1999 12-AUG-1998 Human NCE-2 protein.	365	100
954	AF145615	Drosophila melanogaster	BcDNA.GH03377	823	46
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99
957	AF195623	Homo sapiens	cholinephosphotransferase 1 alpha	2126	99
958	X94917	Drosophila melanogaster	head-elevated expression in 0.9 kb	155	32
959	U54807	Rattus norvegicus	GTP-binding protein	1167	97
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	471	100
962	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
963	AF001754	Homo sapiens	transient receptor potential-related channel 7, a novel putative Ca2+ channel protein	317	30
964	AL035419	Homo sapiens	dJ1100H13.1 (putative novel protein)	1129	100
965	X61381	Rattus rattus	interferon-induced protein	202	46
966	D38169	Homo sapiens	inositol 1,4,5-trisphosphate 3-kinase isoenzyme	3278	100
967	AL031432	Homo sapiens	dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1)	893	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Homo sapiens	guanine nucleotide exchange factor (long isoform)	2752	99
970	AF281134	Homo sapiens	exosome component Rrp46	1186	100
971	U53336	Caenorhabditis elegans	weak similarity over a short region to myosin heavy chain	536	23
972	AC018749	Leishmania major	L8840.12	589	53
973	AF188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens	Tax1 binding protein	852	98
975	AF049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ ID NO: 8101.	626	100
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	908	100
979	U94991	Xenopus laevis	transcription factor XLMO1	795	97
980	S73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo sapiens	Human protein clone HP01462.	2501	100
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH: ubiquinone oxidoreductase complex	964	85
984	AJ249207	Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990	AF161426	Homo sapiens	HSPC308	448	92
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92
993	AL023859	Schizosaccharomyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445_1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930_1.	1340	98
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens	BM-002	428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	2058	100
1005	S45367	Canis familiaris	centractin	1949	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1006	S45367	Canis familiaris	centractin	1315	98
1007	AB022158	Mus musculus	chaperonin containing TCP-1 epsilon subunit	2649	96
1008	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	1282	97
1009	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1010	Z68218	Caenorhabditis elegans	K01H12.1	269	67
1011	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1012	Z14000	Homo sapiens	RING1	2017	100
1013	G02841	Homo sapiens	Human secreted protein, SEQ ID NO: 6922.	332	93
1014	AF145659	Drosophila melanogaster	BcDNA.GH10333	1244	52
1015	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	664	67
1016	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	772	97
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374.	2323	100
1018	X67250	Rattus norvegicus	n-chimaerin	1710	97
1019	AF183417	Homo sapiens	microtubule-associated proteins 1A/1B light chain 3	631	100
1020	AF164795	Homo sapiens	sex-regulated protein janus-a	674	100
1021	AF190625	Coturnix coturnix	qdgl-1	638	96
1022	AL133363	Arabidopsis thaliana	putative protein	155	37
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge	2243	100
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	U80736	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia roretzi	HrPET-1	1048	54
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme isolog	1045	100
1029	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1030	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1031	AF193795	Homo sapiens	vacuolar sorting protein VPS29/PEP11	960	100
1032	AJ222968	Mus musculus	L-periaxin	120	30
1033	Z81317	Schizosaccharomyces pombe	DNA2-NAM7 helicase family protein	685	31
1034	Y41519	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	1321	99
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabditis elegans	H14A12.3 gene product	190	30
1037	U37251	Homo sapiens	Description: KRAB zinc finger protein; this is a splicing supplied by author	196	43
1038	W74580	Homo sapiens	Human membrane protein BA0306.	1921	97
1039	U88173	Caenorhabditis elegans	weak similarity to Arabidopsis thaliana ubiquitin-like protein 8	331	80

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1040	AF296204	Homo sapiens	blood group carrier molecule DOK1	1617	99
1041	Y96730	Homo sapiens	PRO539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	F-box protein FWD2	2397	98
1043	AF151023	Homo sapiens	HSPC189	1104	100
1044	AF181631	Drosophila melanogaster	BcDNA.GH04929	204	37
1045	Y77985	Homo sapiens	Human collectin amino acid sequence.	1940	100
1046	AJ243972	Homo sapiens	6-phosphogluconolactonase	1317	100
1047	AB035863	Homo sapiens	ATP specific succinyl CoA synthetase beta subunit precursor	2324	99
1048	AL034550	Homo sapiens	dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOL4) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte protein 3	634	100
1050	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	868	100
1051	AF190624	Mus musculus	mdg1-1	236	85
1052	AE003529	Drosophila melanogaster	CG6151 gene product	160	44
1053	G01191	Homo sapiens	Human secreted protein, SEQ ID NO: 5272.	646	98
1054	AL162756	Neisseria meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1535	99
1056	U89649	Chlamydomonas reinhardtii	Mr19,000 outer arm dynein light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis-suppressor 1	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like protein pemphaxin	1710	99
1059	AJ270952	Homo sapiens	putative membrane protein	1363	100
1060	AF224263	Heterodontus francisci	HoxD8	742	83
1061	X63417	Homo sapiens	IRLB	1037	100
1062	AL079345	Streptomyces coelicolor A3(2)	hypothetical protein	143	27
1063	Y71112	Homo sapiens	Human Hydrolase protein-10 (HYDRL-10).	2547	100
1064	AF263614	Homo sapiens	acetyl-CoA synthetase	3493	99
1065	Y13356	Homo sapiens	Amino acid sequence of protein PRO221.	1363	100
1066	AC006153	Homo sapiens	similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
1067	Y18930	Sulfolobus solfataricus	hypothetical protein	162	29
1068	R65969	Homo sapiens T98G	Glioblastoma-derived polypeptide.	887	100
1069	Y07964	Homo sapiens	Human secreted protein fragment	863	96
1070	AF177476	Rattus norvegicus	CDK5 activator-binding protein	1995	86
1071	AF245505	Homo sapiens	adlican	3109	99
1072	U92794	Mus musculus	alpha glucosidase II, beta subunit	147	36
1073	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	698	98
1074	U15779	Homo sapiens	p70	380	28
1075	Y13392	Homo sapiens	Amino acid sequence of	1271	91

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein PRO328.		
1076	AF161457	Homo sapiens	HSPC339	571	100
1077	Y79509	Homo sapiens	Human carbohydrate-associated protein CRBAP-5.	2151	98
1078	AF223466	Homo sapiens	HT015 protein	831	66
1079	AL132965	Arabidopsis thaliana	putative WD-40 repeat-protein	286	29
1080	AB024937	Homo sapiens	LUNX	1284	100
1081	Y14768	Homo sapiens	V-ATPase G-subunit like protein	579	100
1082	AF016416	Caenorhabditis elegans	F29A7.4 gene product	141	31
1083	L13291	Homo sapiens	ADP-ribosylarginine hydrolase	802	45
1084	AB041541	Mus musculus	unnamed protein product	151	44
1085	G01922	Homo sapiens	Human secreted protein, SEQ ID NO: 6003.	202	97
1086	AB030814	Homo sapiens	H-REV107 protein homolog	833	100
1087	AF151638	Homo sapiens	phosphatidylcholine transfer protein	1142	100
1088	Y84432	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2783	100
1089	Y94867	Homo sapiens	Human protein clone HP10563.	613	100
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586	Mus musculus	unnamed protein product	1103	81
1092	Y71277	Homo sapiens	Human Zlipo3 protein.	606	100
1093	U34973	Mus musculus	protein tyrosine phosphatase-like	1131	95
1094	Y66677	Homo sapiens	Membrane-bound protein PRO828.	522	56
1095	Y87276	Homo sapiens	Human signal peptide containing protein HSPP-53 SEQ ID NO:53.	1029	99
1096	Y87276	Homo sapiens	Human signal peptide containing protein HSPP-53 SEQ ID NO:53.	863	98
1097	AF161455	Homo sapiens	HSPC337	742	98
1098	U80029	Caenorhabditis elegans	similar to thioredoxin	242	39
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005866	Homo sapiens	Sqv-7-like protein	1118	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1102	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1103	AL110244	Homo sapiens	hypothetical protein	299	31
1104	AF242194	Drosophila melanogaster	brakeless-B	147	52
1105	AL031010	Homo sapiens	dJ422F24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5)	968	100
1106	U28016	Mus musculus	parathion hydrolase (phosphotriesterase)-related protein	1624	87
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	495	98
1109	AF217287	Drosophila melanogaster	G protein RhoBTB	834	54
1110	Y28921	Homo sapiens	Human regulatory protein HRGP-7.	941	48
1111	Y28921	Homo sapiens	Human regulatory protein HRGP-7.	1331	51
1112	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1113	AF182078	Homo sapiens	glioma tumor suppressor candidate region protein 2	2418	100
1114	G04039	Homo sapiens	Human secreted protein, SEQ	475	96

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 8120.		
1115	AF229439	Mus musculus	zinc finger protein 289	1697	91
1116	L40357	Homo sapiens	thyroid receptor interactor	509	100
1117	L40357	Homo sapiens	thyroid receptor interactor	404	85
1118	A12155	Homo sapiens	Human X5L cDNA.	1673	100
1119	AL161542	Arabidopsis thaliana	isomerase like protein	607	53
1120	AL023754	Homo sapiens	dJ272L16.1 (Rat Ca2+/Calmodulin dependent Protein Kinase LIKE protein)	2341	98
1121	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	321	36
1122	Z14122	Xenopus laevis	XLCL2	455	77
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
1125	AL035690	Homo sapiens	dJ202I21.1 (novel protein)	952	100
1126	AJ000217	Homo sapiens	CLIC2	1286	99
1127	AB030505	Mus musculus	UBE-1c2	1069	79
1128	Y73375	Homo sapiens	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccharomyces pombe	putative nuclear pore protein	596	39
1133	Z68197	Schizosaccharomyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange factor	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	Y76219	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo sapiens	A Rab protein designated HRABS-2.	1065	99
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein-Zap70 fusion product.	3309	100
1142	Y13402	Homo sapiens	Amino acid sequence of protein PRO310.	1694	99
1143	G03875	Homo sapiens	Human secreted protein, SEQ ID NO: 7956.	660	99
1144	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	750	98
1145	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	1096	100
1146	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1147	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1148	G02548	Homo sapiens	Human secreted protein, SEQ ID NO: 6629.	570	98
1149	Y73336	Homo sapiens	HTRM clone 2019742 protein sequence.	1492	100
1150	W74841	Homo sapiens	Human secreted protein encoded by gene 113 clone	228	55

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			HEAAR60.		
1151	AF044201	Rattus norvegicus	neural membrane protein 35; NMP35	1570	92
1152	AF156774	Homo sapiens	lysophosphatidic acid acyltransferase-gamma1	1855	99
1153	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	872	64
1154	AF131852	Homo sapiens	Unknown	473	100
1155	Y41705	Homo sapiens	Human PRO352 protein sequence.	1381	97
1156	G04036	Homo sapiens	Human secreted protein, SEQ ID NO: 8117.	607	99
1157	AF112444	Lupinus luteus	L-asparaginase	287	43
1158	AF151848	Homo sapiens	CGI-90 protein	232	32
1159	AJ272267	Homo sapiens	choline dehydrogenase	2449	100
1160	AB001773	Ciona savignyi	PEM-6	196	33
1161	Y87330	Homo sapiens	Human signal peptide containing protein HSPP-107 SEQ ID NO:107.	746	83
1162	Y87333	Homo sapiens	Human signal peptide containing protein HSPP-107 SEQ ID NO:107.	746	83
1163	AF113534	Homo sapiens	HP1-BP74 protein	2723	96
1164	AF232226	Danio rerio	Deddi	191	41
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	1051	71
1166	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	945	76
1167	AF187733	Homo sapiens	syntaphilin	831	42
1168	AB019435	Homo sapiens	phospholipase	951	55
1169	AF064604	Homo sapiens	KE03 protein	324	33
1170	Y01164	Homo sapiens	Polypeptide fragment encoded by gene 6.	1191	100
1171	L03188	Saccharomyces cerevisiae	putative	180	22
1172	AF113751	Mus musculus	nuclear pore membrane glycoprotein POM210	3941	81
1173	AJ245417	Homo sapiens	G5b protein	794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabditis elegans	F33G12.3 gene product	332	28
1176	M35617	Homo sapiens	T-cell receptor V-alpha-J-alpha region	284	83
1177	AC012680	Arabidopsis thaliana	putative protein phosphatase 2C; 55455-56414	209	37
1178	G01345	Homo sapiens	Human secreted protein, SEQ ID NO: 5426.	692	99
1179	AL096767	Homo sapiens	dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)	1342	100
1180	AF039716	Caenorhabditis elegans	similar to ATP synthase B chain	496	55
1181	Y11710	Homo sapiens	collagen type XIV	1048	97
1182	X82240	Homo sapiens) >R94974 R94974 09-MAY-1996 27-OCT-1994 Human TCL-1 polypeptide.	T cell leukemia/lymphoma 1	617	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		(Homo sapiens			
1183	U42841	Caenorhabditis elegans	short region of weak similarity to collagen	161	33
1185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	99
1186	L27645	Danio rerio	growth-associated protein	130	36
1187	Y02738	Homo sapiens	Human secreted protein encoded by gene 89 clone HLHPP03.	636	100
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	182	33
1190	X89602	Homo sapiens	rTSbeta	197	100
1191	U32828	Haemophilus influenzae Rd	ribosomal protein S6 modification protein (rimK)	268	31
1192	AF154831	Rattus norvegicus	PV-1	1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone vc16_1 derived protein.	918	100
1194	AF026530	Rattus norvegicus	stathmin-like-protein splice variant RB3''	1093	97
1195	U35244	Rattus norvegicus	vacuolar protein sorting homolog r-vps33a	2981	96
1196	Y70470	Homo sapiens	Human p53 target molecule, PRG3 protein.	1680	100
1197	AF157310	Homo sapiens	AD-017 protein	912	47
1198	AF125443	Caenorhabditis elegans	contains similarity to S. pombe phosphatidyl synthase (GB:Z28295)	460	39
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	Z85986	Homo sapiens	dJ108K11.3 (similar to yeast suppressor protein SRP40)	1143	75
1203	U18762	Rattus norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002329	Homo sapiens	KIAA0329	151	24
1206	AB019233	Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	742	100
1208	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	Z97630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	181	44
1210	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	Y27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	1267	100
1212	AF117814	Mus musculus	odd-skipped related 1 protein	945	66
1213	AF277233	Naegleria fowleri	calcineurin B	222	39
1214	D14849	Mus musculus	meiosis-specific nuclear structural protein 1	1950	77
1215	G03022	Homo sapiens	Human secreted protein, SEQ ID NO: 7103.	590	100
1216	Z72510	Caenorhabditis	similarity to yeast UTR3	634	49

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		is elegans	protein (Swiss Prot accession yk677h11.5 comes from this gene		
1217	Z49703	Saccharomyces cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	Z70750	Caenorhabditis elegans	similar to vanadate resistance protein transmembranous comes from this gene	965	58
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	Y73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
1229	AF045564	Rattus norvegicus	development-related protein	1715	93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
1231	L08239	Homo sapiens	located at OATL1	2274	100
1232	AF121863	Homo sapiens	sorting nexin 14	1964	100
1233	AF121863	Homo sapiens	sorting nexin 14	1203	84
1234	AC024805	Caenorhabditis elegans	contains similarity to TR:O04595	744	31
1235	AC006634	Caenorhabditis elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated-tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239	AB026264	Homo sapiens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243	X76483	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1246	AJ276003	Homo sapiens	GAR1 protein	1216	100
1247	Y57910	Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
1248	AC004874	Homo sapiens	similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13149	Rattus norvegicus	PAG608	1350	88
1251	M24852	Rattus norvegicus	neuron-specific protein PEP-19	124	46

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1252	AF146738	Rattus norvegicus	testis specific protein	771	83
1253	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 6806.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195_1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA transformylase	1556	88
1257	Z35094	Homo sapiens	SURF-2	1354	97
1258	Y13362	Homo sapiens	Amino acid sequence of protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RPP transforming protein; similar to P14373 (PID:g132517)	1299	100
1260	AC005099	Homo sapiens	match to AI222572 (NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase (AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983	Homo sapiens	Ras-associated protein Rap1	433	97
1265	Y70473	Homo sapiens	Human cyclic nucleotide-associated protein-1 (CNAP-1).	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edp1 protein	1077	64
1268	U97006	Caenorhabditis elegans	C13F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle 68	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272	AF201933	Homo sapiens	DC11	650	100
1273	AF201933	Homo sapiens	DC11	346	98
1274	AL021710	Arabidopsis thaliana	putative protein	348	49
1275	AC004449	Homo sapiens	R33683_3	556	100
1276	Y86295	Homo sapiens	Human secreted protein HL2AG87, SEQ ID NO:210.	1920	100
1277	Y71111	Homo sapiens	Human Hydrolase protein-9 (HYDRL-9).	1576	99
1278	S94421	Homo sapiens	T cell receptor eta-exon	478	100
1279	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	100
1280	AF161380	Homo sapiens	HSPC262	772	100
1281	Y48610	Homo sapiens	Human breast tumour-associated protein 71.	779	100
1282	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	406	35
1283	AK024432	Homo sapiens	FLJ00022 protein	403	35
1284	W96153	Homo sapiens	Human FADD-interacting protein (FIP).	1825	81
1285	AJ001019	Homo sapiens	ring finger protein	1301	100
1286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	PEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	1195	100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	668	93
1290	AB023811	Homo sapiens	TUJA	351	54

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1291	Z73424	Caenorhabditis elegans	C44B9.1	235	36
1292	Y94871	Homo sapiens	Human protein clone HP02551.	1222	100
1293	AF180425	Homo sapiens	retinoblastoma-associated protein RAP140	489	29
1294	G03856	Homo sapiens	Human secreted protein, SEQ ID NO: 7937.	538	99
1295	AF133670	Mus musculus	ARL-6 interacting protein-2	367	51
1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	LIM and cysteine-rich domains protein 1	1997	100
1299	U41023	Caenorhabditis elegans	coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens	basic kruppel like factor	1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus	NELF protein	1409	97
1306	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	932	100
1307	U58755	Caenorhabditis elegans	similar to the mitochondrial carrier family	365	54
1308	AF044774	Homo sapiens	breakpoint cluster region protein 2	2681	99
1309	AL078593	Homo sapiens	dJ210B1.1 (KIAA0580)	267	34
1310	X82693	Homo sapiens	E48 antigen	620	96
1311	Z82263	Caenorhabditis elegans	C47A4.1	283	35
1312	AF131218	Homo sapiens	chromosome 16 open reading frame 5	1493	100
1313	Y41763	Homo sapiens	Human PRO938 protein sequence.	1636	100
1314	AF196972	Homo sapiens	JM24 protein	2239	100
1315	AF053356	Homo sapiens	insulin receptor substrate like protein	228	97
1316	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	100
1317	AF153127	Gallus gallus	SAPK interacting protein	2442	89
1318	AF153127	Gallus gallus	SAPK interacting protein	1477	83
1319	AF153127	Gallus gallus	SAPK interacting protein	1651	86
1320	X56932	Homo sapiens	23 kD highly basic protein	1044	100
1321	AF174605	Homo sapiens] >Y83086 Y83086 09-MAR-2000 28-AUG-1998 F-box protein FBP-19. [Homo sapiens	F-box protein Fbx25	467	70
1322	M61732	Trypanosoma cruzi	neuraminidase	214	24
1323	Y17013	porcine endogenous retrovirus	pol	304	64

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1324	AL138655	Arabidopsis thaliana	putative protein	1174	37
1325	AL138655	Arabidopsis thaliana	putative protein	946	35
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein similar to rat tricarboxylate carrier)	1322	99
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein sequence.	785	96
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.	232	39
1332	Y41741	Homo sapiens	Human PRO704 protein sequence.	1860	100
1333	AF295096	Homo sapiens	zinc-finger protein ZHRK1	411	91
1334	Z82271	Caenorhabditis elegans	Similarity to Mouse kinesin-like protein KIF4 comes from this gene	578	44
1335	AE000810	Methanobacterium thermoautotrophicum	conserved protein	290	43
1336	Y68779	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-11.	1019	91
1337	AB027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabditis elegans	weak similarity to TPR domains	215	40
1339	AE001394	Plasmodium falciparum	protein of the YMR7 family	170	29
1340	X76717	Homo sapiens	MT-11 protein	204	89
1341	AC011914	Arabidopsis thaliana	putative mutT protein; 68398-67881	289	45
1342	AJ276171	Homo sapiens	ASPIC	2122	100
1343	AF187016	Homo sapiens	myosin regulatory light chain interacting protein MIR	2303	99
1344	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	894	35
1345	AF257466	Homo sapiens	N-acetylneuraminic acid phosphate synthase	1880	99
1346	Y25896	Homo sapiens	Human secreted protein fragment encoded from gene 64.	1148	100
1347	AJ272073	Torpedo marmorata	male sterility protein 2-like protein	1664	58
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
1351	G02144	Homo sapiens	Human secreted protein, SEQ ID NO: 6225.	418	100
1352	D90869	Escherichia coli	similar to	2047	100
1353	A12029	Homo sapiens	MRP-14	613	100
1354	AC005328	Homo sapiens	R26660_1, partial CDS	870	74
1355	AC024876	Caenorhabditis elegans	contains similarity to SW:RPB1_CRIGR	829	61
1356	AF077226	Homo sapiens	copine III	1876	64
1359	AF217188	Mus musculus	YIP1B	801	63
1360	AC074331	Homo sapiens	ZNF234	3869	100
1361	AL163279	Homo sapiens	homolog to cAMP response	5035	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			element binding and beta transducin family proteins		
1362	Z48475	Homo sapiens	glucokinase regulator	3160	99
1363	Z48475	Homo sapiens	glucokinase regulator	2682	97
1364	AF195764	Homo sapiens	megakaryocyte-enhanced gene transcript 1 protein; MEGT1 protein	2055	99
1365	AF116609	Homo sapiens	PRO0915	581	100
1366	AF116609	Homo sapiens	PRO0915	581	100
1367	AL117352	Homo sapiens	dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:Q22557))	2581	99
1368	Y34124	Homo sapiens	Human potassium channel K+Hnov15.	1342	100
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus subtilis	YtaG	429	45
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	PLASH	10253	100
1374	U20286	Rattus norvegicus	lamina associated polypeptide 1C	1567	69
1375	U53445	Homo sapiens	DOC1	1645	46
1376	AL117337	Homo sapiens	bA393J16.1 (zinc finger protein 33a (KOX 31))	250	60
1377	AC005328	Homo sapiens	R26660_1, partial CDS	1126	100
1378	U35113	Homo sapiens	metastasis-associated gene	1823	69
1379	L15313	Caenorhabditis elegans	putative	858	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus	G beta-like protein GBL	1721	96
1384	AF237676	Mus musculus	G beta-like protein GBL	1043	70
1385	Y58793	Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386	AF212162	Homo sapiens	ninein	10369	99
1387	AL031685	Homo sapiens	dJ963K23.2 (novel protein)	337	33
1388	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	1208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour-associated protein 72.	817	99
1401	AC004472	Homo sapiens	PI.11659_5	280	54
1402	X91489	Saccharomyces cerevisiae	putative HMG box	164	27

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1403	Y79222	Homo sapiens	Human transferase TRNSF8-14.	2842	100
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus	ITM	194	29
1406	AB030251	Homo sapiens	GTPase activating protein	3233	99
1407	AJ010585	Rattus rattus	PTB-like protein	2684	99
1408	X75760	Drosophila melanogaster	LRR47	364	29
1409	U76618	Mus musculus	N-RAP	804	48
1410	AC005578	Homo sapiens	P20887_1, partial CDS	835	63
1411	AE000284	Escherichia coli	orf, hypothetical protein.	360	100
1412	X01563	Escherichia coli	L5 (=plE) (aa 1-179)	911	100
1413	W76279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	organic anion transporter OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1416	AF097994	Homo sapiens	L-kynurenine/alpha-aminoadipate aminotransferase	2202	99
1417	AF151077	Homo sapiens	HSPC243	1262	99
1418	Y09945	Rattus norvegicus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus auratus	guanine nucleotide-binding protein beta 5	2179	76
1420	AL162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel protein, presumed ortholog of mouse K-Cl cotransporter KCC2))	5696	100
1421	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	152	29
1422	Y94923	Homo sapiens	Human secreted protein clone qs14_3 protein sequence SEQ ID NO:52.	4039	99
1423	AF179388	Homo sapiens	cancer-amplified transcriptional coactivator ASC-2	10748	99
1424	Y48517	Homo sapiens	Human breast tumour-associated protein 62.	1851	99
1425	AF208848	Homo sapiens	BM-006	1454	89
1426	AF208848	Homo sapiens	BM-006	853	79
1427	AF112886	Bos taurus	differentiation enhancing factor 1	4693	95
1428	U41387	Homo sapiens	Gu protein	1372	63
1429	AF161534	Homo sapiens	HSPC049	2853	78
1430	AF125043	Mus musculus	bisphosphate 3'-nucleotidase	275	30
1431	Y66718	Homo sapiens	Membrane-bound protein PRO1106.	1886	100
1432	AF193613	Homo sapiens	cell recognition molecule Caspr2	568	100
1433	AB044560	Mus musculus	Gliacolin	192	34
1434	R99800	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of nerve cells.	707	51
1435	AF220530	Homo sapiens	myo-inositol 1-phosphate synthase A1	2904	100
1436	X70944	Homo sapiens	PTB-associated splicing factor	1261	72
1437	AF271732	Homo sapiens	bridging integrator-3	1282	100
1438	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	595	98
1439	AJ293659	Homo sapiens	mucolipidin	628	97
1440	AF219138	Homo sapiens	GGA3 long isoform	3083	100
1441	AF219138	Homo sapiens	GGA3 long isoform	3346	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1442	AB039669	Homo sapiens	ALEX3	1944	100
1443	AF237711	Drosophila melanogaster	Diablo	191	27
1444	AJ011896	Homo sapiens	Naf1 beta protein	439	39
1445	X73874	Homo sapiens	phosphorylase kinase	6233	98
1446	AF214114	Homo sapiens	breast carcinoma-associated antigen BCAA	3999	99
1447	AF003924	Homo sapiens	ANC_2H01	2645	99
1448	AF003136	Caenorhabditis elegans	contains weak similarity to an AMP-binding motif	2843	52
1449	AF155112	Homo sapiens	NY-REN-50 antigen	1184	89
1450	Y95004	Homo sapiens	Human secreted protein vc54_1, SEQ ID NO:49.	985	100
1451	AF107203	Homo sapiens	ataxin 2-binding protein	688	57
1452	AF107203	Homo sapiens	ataxin 2-binding protein	456	78
1453	Z38011	Mus musculus	DMR-N9	882	56
1454	X90568	Homo sapiens	Protein sequence and annotation available soon via LABEIT@EMBL-Heidelberg.DE	510	28
1455	AL035409	Homo sapiens	dJ564M11.3 (similar to sialyltranferase)	1356	100
1456	D44480	Mus musculus	MATH-2 protein	272	100
1458	AF141326	Homo sapiens	RNA helicase-HDB/DICE1	478	45
1459	AF242552	Gallus gallus	retinovin	945	34
1460	U11036	Homo sapiens	Ibd1	724	84
1461	AB025258	Mus musculus	granuphilin-a	545	39
1462	Y08134	Homo sapiens	acid sphingomyelinase-like phosphodiesterase	2428	99
1463	AC004997	Homo sapiens	match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333)	869	98
1464	AC004997	Homo sapiens	match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333)	869	98
1465	U32743	Haemophilus influenzae Rd	fucose operon protein (fucU)	315	50
1466	Y09022	Homo sapiens	Not56-like protein	2342	100
1467	AC003034	Homo sapiens	Homolog of rat kidney-specific (KS) gene	1072	99
1468	AF071544	Spinacia oleracea (	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	333	26
1469	Y57930	Homo sapiens	Human transmembrane protein HTMPN-54.	1053	100
1470	AF032666	Rattus norvegicus	rsec5	4504	93
1471	Y70467	Homo sapiens	Human membrane channel protein-17 (MECHP-17).	452	74
1472	AL031033	Homo sapiens	C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)	1694	100
1473	AF177292	Homo sapiens	genethonin 3	4026	98
1474	S45936	Homo sapiens	HTS1	1101	50
1475	Y86241	Homo sapiens	Human secreted protein HOABR60, SEQ ID NO:156.	1879	98
1476	AJ010317	Fugu rubripes	Sand	1278	68
1477	U42831	Caenorhabditis elegans	coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157)	846	44
1478	X62447	Homo sapiens	PR 264	543	61
1479	X82209	Homo sapiens	MN1	7116	100
1480	U10536	Pan paniscus	MHC class I A	675	84

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:F91086))	1274	65
1482	Z98977	Schizosaccharomyces pombe	putative vacuolar protein	256	29
1483	AB005662	Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878	Homo sapiens	DNA binding protein	1006	53
1486	Y69161	Homo sapiens	Amino acid sequence of a partial protein kinase.	575	99
1487	X84156	Saccharomyces cerevisiae	ATH1	341	29
1488	AF038963	Homo sapiens	RNA helicase	446	34
1489	U56966	Caenorhabditis elegans	coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3	620	42
1490	AE000989	Archaeoglobus fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	M80633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	462	37
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	Y94897	Homo sapiens	Human protein clone HP10574.	1371	100
1496	AL049699	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1497	AF037447	Homo sapiens	ribosomal S6 protein kinase	2427	100
1498	AL445067	Thermoplasma acidophilum	putative target YPL207w of the HAP2 transcriptional complex related protein	269	35
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500	AJ277750	Homo sapiens	UBASH3A protein	3509	100
1501	AL050333	Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1502	AF179896	Homo sapiens	TALE homeobox protein Meis2b	1140	100
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2a	1177	100
1504	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	1442	99
1505	X82494	Homo sapiens	fibulin-2	3580	99
1506	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548	Homo sapiens	dJ1103G7.6 (novel protein)	1090	100
1508	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1736	100
1509	AF220182	Homo sapiens	uncharacterized hypothalamus protein HT008	1181	98
1510	U64601	Caenorhabditis elegans	Gene probably begins in the next cosmid	415	58
1511	AL356192	Neurospora crassa	related to MDM1 protein	196	29
1512	D17629	Homo sapiens	N-acetylgalactosamino 6-sulfate sulfatase (GALNS)	1829	100
1513	AF160717	Homo sapiens	x 009 protein	694	99
1514	AJ243531	Homo sapiens	nM15 protein	735	100
1515	AC003672	Arabidopsis thaliana	putative C3HC4-type RING zinc finger protein	407	30
1516	AF115435	Rattus norvegicus	syntaxin 17	1374	90
1517	AF003140	Caenorhabditis elegans	C44E4.5 gene product	274	31
1518	AB002584	Rattus norvegicus	beta-alanine-pyruvate aminotransferase	2238	82
1519	AL121764	Schizosaccha	yeast atp12 protein precursor	270	30

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		romyces pombe	homolog		
1520	AF255910	Homo sapiens	vascular endothelial junction-associated molecule	547	100
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo sapiens	Membrane-bound protein PRO190.	985	100
1523	Y94450	Homo sapiens	Human inflammation associated protein	250	43
1524	AC000107	Arabidopsis thaliana	F17F8.22	277	37
1525	AF109377	Mus musculus	1d1Bp	1277	83
1526	AL031427	Homo sapiens	dJ167A19.4 (novel protein)	1432	99
1527	Y08135	Mus musculus	acid sphingomyelinase-like phosphodiesterase	1496	79
1528	AK024423	Homo sapiens	FLJ00012 protein	611	100
1529	AF154502	Homo sapiens	quiescent cell proline dipeptidase	679	100
1530	AF205598	Homo sapiens	transposase-like protein	1368	100
1531	AF251039	Homo sapiens	putative zinc finger protein	1420	50
1532	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	493	57
1533	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis thaliana	F23N19.9	374	37
1535	AB027564	Homo sapiens	DINB1	4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	Y50907	Homo sapiens	Human fetal brain cDNA clone vb3_1 derived protein.	3693	99
1538	AF017368	Mus musculus	faciogenital dysplasia protein 2	177	47
1539	AF266756	Homo sapiens	sphingosine kinase	2011	99
1540	Z48804	Homo sapiens	OA1	2238	100
1541	AF000195	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1	379	42
1542	Y71159	Homo sapiens	Human phosphodiesterase interacting protein, myomegalin.	9415	99
1543	X76092	Homo sapiens	DNA binding protein RPX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
1545	AF198487	Homo sapiens	transcription factor LBP-1b	2022	100
1546	AF016417	Caenorhabditis elegans	Similar to BZIP transcription factor	518	42
1547	X55885	Homo sapiens	KDEL receptor	1106	100
1548	AB035495	Carassius auratus	ubiquitin-activating enzyme E1	836	42
1549	AL021707	Homo sapiens	dJ508I15.4 (KIAA0668)	3688	100
1550	AJ223978	Bacillus subtilis	YvqK protein	292	42
1551	AF145615	Drosophila melanogaster	BcDNA.GH03377	822	44
1552	AL157734	Schizosaccharomyces pombe	putative mannosyltransferase involved in N-glycosylation	435	37
1553	AF079527	Mus musculus	IER5	691	63
1554	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	1099	88
1555	Y44722	Homo sapiens	Human immune system molecule, ISMO-3.	1780	99
1556	AF116553	Drosophila melanogaster	antennal-specific short-chain dehydrogenase/reductase	277	32
1557	Y71056	Homo sapiens	Human membrane transport	1975	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein, MTRP-1.		
1558	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.	1975	99
1559	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.	1894	97
1560	AF092050	Mus musculus	beta-1,3-N-acetylglucosaminyltransferase	262	44
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein ACR5S (similar to rat sperm antigen 4 (SPAG4)))	1607	97
1562	AJ131890	Homo sapiens	DNA polymerase lambda	3002	100
1563	AL035424	Homo sapiens	dA22D12.1 (novel protein similar to Drosophila Kelch proteins)	3015	100
1564	AC002400	Homo sapiens	Gene product with similarity to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216_1	919	82
1566	AF000195	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1	550	45
1567	AB033281	Homo sapiens	F-box and WD-repeats protein beta-TRCP2 isoform C	2879	100
1568	D49473	Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388	100
1572	AE003831	Drosophila melanogaster	CG18445 gene product	180	31
1573	AF074603	Streptomyces griseus subsp. griseus	NonP	205	38
1574	U28993	Caenorhabditis elegans	F22D3.3 gene product	144	27
1575	AF129507	Homo sapiens	transcription factor YCBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila melanogaster	Diablo	421	54
1578	G00975	Homo sapiens	Human secreted protein, SEQ ID NO: 5056.	480	100
1579	AF248744	Cryptosporidium parvum	thrombospondin-related adhesive protein	123	33
1580	AL121782	Homo sapiens	dJ585I14.2 (novel protein (translation of cDNA Em:AK000219))	663	100
1581	AF041853	Homo sapiens	kinesin family member protein KIF3A	345	33
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	100
1583	AE001903	Thermotoga maritima	glycerate kinase, putative	349	34
1584	AF252283	Homo sapiens	Kelch-like 1 protein	3973	100
1585	AF169675	Homo sapiens	leucine-rich repeat transmembrane protein FLRT1	3494	99
1586	AF118274	Homo sapiens	DNb-5	2628	97
1587	X79440	Homo sapiens	NADP+-dependent malic enzyme	3167	99
1588	X99802	Homo sapiens	ZYG homologue	3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	181	47
1591	Z25535	Homo sapiens	nuclear pore complex protein hnup153	7567	99
1592	X13293	Homo sapiens	B-myb protein (AA 1-700)	3678	99
1593	M74027	Homo sapiens	mucin	242	27
1594	AL139314	Schizosaccharomyces	hypothetical protein	235	54

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		pombe			
1595	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
1596	Y94906	Homo sapiens	Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.	2236	98
1597	AF174605	Homo sapiens	F-box protein Fbx25	1408	99
1598	AB032254	Homo sapiens	bromodomain adjacent to zinc finger domain 2A	9676	98
1599	X73114	Homo sapiens	slow MyBP-C	5568	95
1600	X82200	Homo sapiens	gpStaf50	2305	100
1601	Y00876	Homo sapiens	Human LAPH-1 protein sequence.	1149	98
1602	AJ223351	Homo sapiens	HIRA-interacting protein 3	2821	99
1603	AJ222801	Homo sapiens	neutral sphingomyelinase	2268	99
1604	AJ222801	Homo sapiens	neutral sphingomyelinase	1601	99
1605	AF185576	Mus musculus	POZ/zinc finger transcription factor ODA-8	3435	97
1606	AF093744	Homo sapiens	unknown	131	100
1607	A12142	synthetic construct	IFN-pseudo-omega 2	800	98
1608	Y57949	Homo sapiens	Human transmembrane protein HTMPN-73.	1868	100
1609	AF151044	Homo sapiens	HSPC210	681	97
1610	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1611	Y08200	Homo sapiens	rab geranylgeranyl transferase	2976	100
1612	AF220560	Homo sapiens	B/K protein	2486	99
1613	AC004481	Arabidopsis thaliana	nodulin-like protein	371	26
1614	Y09501	Homo sapiens	NADH-cytochrome-b5 reductase	1607	100
1615	Y15521	Homo sapiens	start position 1	3150	97
1616	AJ010750	Rattus norvegicus	Castration induced prostatic apoptosis related protein-1, (CIPAR-1)	890	62
1617	X58079	Homo sapiens	S100 alpha protein	481	100
1618	Y66678	Homo sapiens	Membrane-bound protein PRO1009.	967	100
1619	AJ242973	Homo sapiens	peptide methionine sulfoxide reductase	929	100
1620	AF150733	Homo sapiens	AD-014 protein	288	100
1621	AJ007509	Homo sapiens	E1B-55kDa-associated protein	4646	98
1622	X64177	Homo sapiens	metallothionein	380	100
1623	AE001045	Archaeoglobus fulgidus	A. fulgidus predicted coding region AF0859	240	36
1624	AL355013	Schizosaccharomyces pombe	mitochondrial carrier protein	403	34
1625	Y66746	Homo sapiens	Membrane-bound protein PRO1198.	1184	100
1626	D90053	Sus scrofa	destrin	863	100
1627	Y35954	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 203.	756	100
1628	AL031775	Homo sapiens	dJ30M3.2 (novel protein)	470	100
1629	AF132484	Mus musculus	unknown	286	68
1630	AF017096	Drosophila melanogaster	similar to C. elegans R10H10.6 and S. cerevisiae YD8419.03c	493	61
1631	X03077	Homo sapiens	lactate dehydrogenase-A	1704	100
1632	AF151084	Homo sapiens	HSPC250	763	100
1633	AJ001874	Homo sapiens	orf	255	97
1634	AC012187	Arabidopsis thaliana	Contains weak similarity to GATA-6 DNA-binding protein gb|H36135, gb|Z26200 come from this gene.	143	38

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATRRMAN SCORE	% IDENTITY
1635	AF026246	Homo sapiens	HERV-E integrase	411	90
1636	Y50943	Homo sapiens	Human adult brain cDNA clone ve8_1 derived protein.	1126	95
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	96
1639	Y94942	Homo sapiens	Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90.	1320	100
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	M19351	Mus musculus	Immunoglobulin heavy chain binding protein	145	34
1643	Y70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box protein FBW5	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-1	4456	99
1647	M63180	Homo sapiens	threonyl-tRNA synthetase	1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyostelium discoideum	myoM	297	32
1657	Y28919	Homo sapiens	Human regulatory protein, HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccharomyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3 chain	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein 2	2774	100
1665	Z48613	Saccharomyces cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191_1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Peptide, 370	p40	397	43

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		aa			
1669	Z99753	Schizosaccharomyces pombe	putative NOL1-NOP2-sun family nucleolar protein	569	47
1670	G03130	Homo sapiens	Human secreted protein, SEQ ID NO: 7211.	427	97
1671	M96625	Gallus gallus	cardiac muscle tensin	1185	54
1672	AF174482	Homo sapiens	polycomb 3	2005	99
1673	Y51846	Homo sapiens	Human 18.1 homolog protein fragment.	233	29
1674	AF255334	Homo sapiens	EXP35	152	29
1675	Y94867	Homo sapiens	Human protein clone HP10563.	109	30
1676	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	3043	99
1677	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	1580	91
1678	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1679	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1680	AK024453	Homo sapiens	FLJ00045 protein	1349	100
1681	AF019236	Dictyostelium discoideum	TipD	613	34
1682	AJ243459	Leishmania major	proteophosphoglycan	153	26
1683	Z69369	Schizosaccharomyces pombe	putative GTP-binding protein	560	46
1684	X94910	Homo sapiens	ERp28	1334	100
1685	AF286475	Takifugu rubripes	retinitis pigmentosa GTPase regulator-like protein	196	19
1686	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	100
1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila melanogaster	heat shock protein	138	43
1690	AF240463	Rattus norvegicus	LIS1-interacting protein NUDE1	1383	83
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	60
1693	AF177942	Xenopus laevis	katanin p60	1664	66
1694	AF263539	Homo sapiens	arginine N-methyltransferase	1774	100
1695	AF222689	Homo sapiens	protein arginine N-methyltransferase 1-variant 2	1182	81
1696	AK000193	Homo sapiens	unnamed protein product	1060	100
1697	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	3122	100
1698	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	2181	100
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens	Human ARF-Related Protein-1 (HARP-1).	938	97
1701	AK022407	Homo sapiens	unnamed protein product	315	98
1702	AB024574	Homo sapiens	GTP-binding like protein 2	1172	100
1703	AF055078	Homo sapiens	zinc finger protein 42	421	52
1704	AF198092	Mus musculus	RP42	1057	77
1705	AE003573	Drosophila melanogaster	CG12474 gene product	161	33
1706	AB036345	Drosophila melanogaster	aquaporin	164	24
1707	Y55927	Homo sapiens	Human STLK2 protein.	2146	100
1708	U27121	Danio rerio	G12	212	47
1709	AL391710	Arabidopsis	putative protein	505	50

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		thaliana			
1710	B01311	Homo sapiens	Human PRO241 polypeptide.	1649	97
1711	U40750	Mus musculus	formin binding protein 30	4561	85
1712	AJ011118	Mus musculus	skeletal muscle and cardiac protein	1490	89
1713	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	4416	99
1714	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	2960	100
1715	U08227	Rattus norvegicus	Ras-related protein	511	51
1716	AF168795	Rattus norvegicus	schlafen-4	1129	44
1717	AF196304	Homo sapiens	SUMO-1-specific protease	5804	99
1718	AL355737	Homo sapiens	HMG20A	1782	100
1719	AB029333	Halocynthia roretzi	HrPET-1	1069	46
1720	AF071317	Mus musculus	COP9 complex subunit 7b	1297	97
1721	AJ272215	Homo sapiens	HEYL protein	1681	99
1722	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
1723	AL032643	Caenorhabditis elegans	similar to Uncharacterized protein family UPF0034.	825	41
1724	G01972	Homo sapiens	Human secreted protein, SEQ ID NO: 6053.	586	92
1725	Y94441	Homo sapiens	Human Adipose Specific Protein 1.	1231	100
1726	AF255443	Homo sapiens	CGI-201 protein	4397	99
1727	AF183426	Homo sapiens	HT004 protein	1810	99
1728	D10884	Bos taurus	neurocalcin	1002	99
1729	Z18529	Gallus gallus	tensin	1411	84
1730	Z73423	Caenorhabditis elegans	cDNA EST EMBL:Z14908 comes from this gene-cDNA EST this gene	233	41
1732	AF090891	Homo sapiens	PRO0105	470	30
1733	AJ277724	Homo sapiens	histone deacetylase 8	2015	100
1734	G04050	Homo sapiens	Human secreted protein, SEQ ID NO: 8131.	503	95
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1736	AF096709	Drosophila virilis	failed axon connections protein	276	32
1737	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabditis elegans	contains similarity to Pfam family PF01772 N=1	206	37
1739	X54618	Listeria monocytogenes	phosphadidylinositol specific phospholipase C	134	27
1740	AL031658	Homo sapiens	dJ310G13.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins)	123	31
1741	Y35924	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 173.	1013	99
1742	AC013354	Arabidopsis thaliana	F15H18.15	202	32
1743	W75771	Homo sapiens	Human GTP binding protein APD08.	1932	59
1744	W75771	Homo sapiens	Human GTP binding protein APD08.	1854	61
1745	AF221098	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A	1224	70
1746	Y99372	Homo sapiens	Human PRO1450 (UNQ736) amino acid sequence SEQ ID NO:116.	1332	99
1747	Y94294	Homo sapiens	Human coenzyme A-utilising	842	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			enzyme CoAEN-2.		
1748	AK024436	Homo sapiens	FLJ00026 protein	1619	100
1749	AE000877	Methanobacterium thermoautotrophicum	conserved protein	231	36
1750	AF101361	Drosophila melanogaster	Abnormal X segregation	193	33
1751	Y15067	Homo sapiens	ZNF232	889	100
1752	AF251038	Homo sapiens	GAP-like protein	822	100
1753	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	352	57
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger protein)	2765	100
1757	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase	2020	99
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1759	AF117553	Homo sapiens	double homeobox protein	375	54
1760	Y12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ68EC3.2 (nucleolar protein hNop56)	2595	99
1762	AC002394	Homo sapiens	Gene product with similarity to dynein beta subunit	1542	51
1763	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	877	100
1764	U91541	Homo sapiens	human formiminotransferase cyclodeaminase (ftcd)protein, carboxy-terminal end	596	100
1765	AB013365	Bacillus halodurans	YlqF	350	34
1766	Y38421	Homo sapiens	Human secreted protein encoded by gene No. 36.	145	71
1767	AC009176	Arabidopsis thaliana	putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	216	27
1768	AK000647	Homo sapiens	unnamed protein product	737	99
1769	AJ238982	Homo sapiens	VNN3 protein	2665	99
1770	U73522	Homo sapiens	AMSH	1214	56
1771	U89435	Mus musculus	unknown	829	86
1772	S70011	Rattus sp.	tricarboxylate carrier	1604	95
1773	AL035086	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
1774	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	1057	99
1775	AF110330	Homo sapiens	glutaminase	3146	100
1776	AJ269529	Homo sapiens	glycerol 3-phosphate permease	2787	100
1777	Z81579	Caenorhabditis elegans	cDNA EST yk76f1.5 comes from this gene	232	31
1778	AY007239	Homo sapiens	monooxygenase X	1875	99
1779	AL109608	Schizosaccharomyces pombe	oxysterol-binding protein family	644	38
1780	AF254260	Homo sapiens	tuftelin 1	1729	100
1781	L07924	Mus musculus	guanine nucleotide dissociation stimulator	247	50
1782	AF295773	Homo sapiens	ral guanine nucleotide dissociation stimulator	142	49
1783	AK024475	Homo sapiens	FLJ00068 protein	4333	100
1784	AK024475	Homo sapiens	FLJ00068 protein	3996	93
1785	G03933	Homo sapiens	Human secreted protein, SEQ ID NO: 8014.	570	100
1786	S82637	Homo sapiens	Ig lambda-like gene/beta-	247	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT401!.DOC)

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e-12 157-181
3	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 8.085e-13 358-381
4	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.400e-10 1129-1146 BL00028 16.07 1.257e-09 820-837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
6	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
7	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e-09 863-917
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e-12 294-312 PR00464G 12.41 4.231e-11 377-393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e-09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e-10 89-99 PF00023B 14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e-09 79-113
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.868e-10 517-535 PR00208A 12.59 2.233e-09 520-538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-14 282-295 PD00066 13.92 9.400e-14 477-490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e-13 254-267 PD00066 13.92 1.429e-12 393-406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	BL00845 16.43 2.200e-25 55-80
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 348-390
22	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-26 302-333

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-26 302-333
25	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115T 8.45 7.271e-29 1208-1242 BL00115Q 18.08 2.776e-21 953-983 BL00115Y 11.86 8.000e-17 1604-1650 BL00115M 19.19 8.130e-16 731-774 BL00115H 14.34 9.392e-16 463-496 BL00115A 15.44 7.414e-15 43-82 BL00115R 6.50 6.128e-14 983-1010 BL00115J 16.71 9.289e-14 591-617 BL00115I 8.33 4.336e-13 535-590 BL00115L 12.25 5.939e-13 662-694 BL00115G 11.65 6.011e-13 435-463 BL00115K 15.03 3.417e-10 617-659 BL00115O 16.76 5.805e-10 863-913 BL00115P 11.54 7.538e-10 913-953 BL00115S 18.24 7.968e-10 1010-1052 BL00115U 10.34 4.475e-09 1242-1265
26	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 4.109e-11 81-110 BL00420A 20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23 proteins.	BL00050A 23.71 9.250e-27 94-127 BL00050B 14.81 8.125e-12 133-147
28	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925B 3.73 3.089e-10 41-54
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e-09 486-516
32	BL00557	FMN-dependent alpha-hydroxy acid dehydrogenases proteins.	BL00557D 17.76 5.065e-37 274-316 BL00557A 35.08 8.909e-29 24-73 BL00557C 15.59 1.000e-28 227-257 BL00557B 21.27 8.898e-22 130-169
34	PR00629	SHC PHOSPHOTYROSINE INTERACTION DOMAIN SIGNATURE	PR00629E 9.90 5.886e-35 299-328 PR00629F 10.95 8.364e-32 334-361 PR00629B 13.66 3.786e-27 224-247 PR00629A 13.45 8.364e-21 206-222 PR00629C 3.80 4.000e-12 249-261 PR00629D 12.45 3.739e-11 276-286
35	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131 PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166
36	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166
37	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e-10 264-298
38	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e-10 264-298
39	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e-10 264-298
40	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380B 12.64 7.366e-14 342-360 PR00380C 13.18 6.927e-13 375-394 PR00380D 9.93 2.180e-12 429-451 PR00380A 14.18 5.154e-12 143-165
44	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-40 239-290 BL00345A 13.95 2.452e-14 204-223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-40 215-266 BL00345A 13.95 2.452e-14 180-199
46	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551A 15.63 3.538e-26 172-202 DM01551C 14.62 3.571e-17 232-252 DM01551B 8.84 4.750e-11 214-226
47	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 9.328e-11 246-260
48	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.231e-33 6-45
50	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e-19 994-1019 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1020-1042 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312
51	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e-19 990-1015 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1016-1038 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312
52	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.063e-14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e-17 20-38 PR00988F 12.23 7.828e-15 196-210 PR00988C 13.64 6.108e-14 104-120 PR00988E 8.27 3.872e-11 174-186 PR00988D 5.95 6.878e-10 160-171 PR00988B 11.60 2.915e-09 57-69
55	PR00762	CHLORIDE CHANNEL SIGNATURE	PR00762C 9.29 4.682e-21 294-314 PR00762D 11.29 4.103e-19 509-530 PR00762A 14.22 9.333e-18 199-217

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00762F 15.12 3.100e-16 563-583 PR00762B 12.12 6.063e-16 230-250 PR00762E 12.07 2.286e-15 545-562 PR00762G 14.13 6.276e-13 601-616
56	BL00216	Sugar transport proteins.	BL00216B 27.64 8.800e-10 153-203
58	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.049e-10 1080-1135
59	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.049e-10 1062-1117
61	PD01929	KINASE TYPE RESISTANCE ANTIBIOTIC TRANSFERASE AM.	PD01929E 10.76 9.018e-09 206-221
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-09 680-693
69	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-09 670-683
70	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.714e-10 51-64
72	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e-09 108-118
73	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 7.075e-12 118-166
74	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 6.116e-10 93-120
76	DM00471	0 PROKARYOTIC DNA TOPOISOMERASE I.	DM00471A 11.73 9.357e-13 53-66 DM00471B 8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e-13 223-236 PD02876D 12.13 2.588e-12 334-351
81	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e-13 282-295 PD02876D 12.13 2.588e-12 393-410
83	BL00708	Prolyl endopeptidase family serine proteins.	BL00708B 24.91 7.197e-12 570-601
84	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 8.043e-09 985-1004
86	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 1.379e-09 246-269
89	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.200e-09 264-279 PR00320D 12.19 8.650e-09 264-279
93	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 2.588e-14 316-332
95	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.000e-10 123-154
96	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.000e-10 212-243
97	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.318e-13 134-146 PR00081A 10.53 2.500e-12 54-72
98	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 5.500e-24 401-423 PR00380D 9.93 7.188e-20 613-635 PR00380B 12.64 7.517e-16 529-547 PR00380C 13.18 2.756e-13 560-579

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
102	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 7.545e-14 289-308
104	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.786e-18 298-314 BL00479A 19.86 4.913e-16 155-178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294e-12 181-197
106	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.011e-12 43-83
107	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 5.000e-16 403-416
108	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191K 17.38 4.951e-27 238-282 BL00191J 11.37 6.447e-17 182-204
109	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.938e-37 8-47
110	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 8.297e-10 38-50
113	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 5.800e-23 156-187 BL00107B 13.31 9.100e-14 225-241
117	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 1.000e-17 46-91 BL00214A 21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 8.560e-13 36-67
119	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529C 11.03 7.506e-10 158-177
120	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-09 80-95
121	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-09 80-95
127	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 7.158e-13 216-241
128	BL01032	Protein phosphatase 2C proteins.	BL01032C 6.14 3.195e-12 147-157 BL01032H 11.25 5.680e-11 318-331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902e-09 379-389
129	BL01310	ATPIG1 / PLM / MAT8 family proteins.	BL01310 14.74 6.694e-26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e-15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e-09 119-133
133	BL00880	Acyl-CoA-binding protein.	BL00880 17.52 5.575e-26 72-122
134	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 9.308e-14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e-10 475-496
136	BL01310	ATPIG1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e-29 71-107
140	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e-14 214-231 BL00028 16.07 9.471e-14 102-119 BL00028 16.07 2.800e-13 18-35

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 5.500e-13 74-91 BL00028 16.07 9.100e-13 186-203 BL00028 16.07 8.043e-12 46-63 BL00028 16.07 8.435e-12 130-147 BL00028 16.07 9.217e-12 270-287 BL00028 16.07 6.192e-11 242-259 BL00028 16.07 4.000e-10 158-175
141	BL00501	Signal peptidases I serine proteins.	BL00501D 16.69 9.538e-14 113-133 BL00501C 9.61 8.688e-10 89-101
143	BL01020	SAR1 family proteins.	BL01020C 15.35 7.722e-20 79-130
146	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.400e-25 335-374
149	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126C 22.07 1.450e-25 509-550 BL00126E 35.22 3.951e-16 654-709 BL00126D 25.50 1.360e-15 565-604 BL00126B 15.20 8.200e-11 483-495 BL00126A 27.56 8.269e-11 442-479
151	BL00632	Ribosomal protein S4 proteins.	BL00632 23.79 5.271e-20 106-149
154	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 5.304e-19 29-58 BL00559K 13.17 2.957e-18 172-199 BL00559J 19.63 8.385e-13 99-151 BL00559L 13.60 5.814e-12 241-259
155	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.692e-13 13-35
157	BL00406	Actins proteins.	BL00406D 12.58 1.547e-18 275-330 BL00406A 9.95 5.776e-16 15-50 BL00406B 5.47 7.429e-12 69-124 BL00406C 6.75 9.682e-12 128-183
160	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132A 26.07 7.000e-14 22-63 BL00132C 21.35 3.466e-12 104-145
165	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.043e-13 139-158
168	BL00362	Ribosomal protein S15 proteins.	BL00362 24.67 9.700e-15 129-172
169	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 1.000e-35 640-686 BL00039A 10.44 1.964e-13 212-251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e-12 465-489
175	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.721e-12 14-36
178	BL01310	ATPIG1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e-29 133-169
179	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 9.455e-36 6-45

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		BINDING NU.	
180	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 7.429e-20 160-180 PR00007A 19.33 4.938e-19 133-160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e-11 238-249
181	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 280-323
182	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 263-306
183	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 280-323
184	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 263-306
188	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e-09 460-471
189	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e-09 440-451
190	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383F 15.51 7.188e-17 666-682 BL00383A 13.34 8.714e-17 162-177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e-14 628-639 BL00383F 15.51 1.720e-13 371-387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e-13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e-09 509-520 BL00383D 11.92 4.000e-09 589-602 BL00383B 7.61 8.000e-09 479-488
191	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 7.911e-15 83-105 PR00450C 12.22 6.286e-13 47-69
193	PF00564	Octicosapeptide repeat proteins.	PF00564B 24.74 6.164e-16 227-278
194	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 9.156e-15 204-224 PR00503B 9.96 9.571e-13 170-187
195	BL00901	Cysteine synthase/cystathionine beta-synthase P-phosphate att.	BL00901C 20.63 3.429e-18 67-117
197	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e-17 40-57 BL00636B 15.11 2.000e-13 67-88
198	PR00690	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e-09 463-482
199	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 2.343e-12 84-130
201	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.352e-12 509-522
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e-10 39-72
206	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PR00261A 11.02 4.462e-19 65-87 PR00261C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e-18 65-87 PR00261B 14.12 4.000e-18 143-165 PR00261A 11.02

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			4.833e-18 143-165 PR00261D 12.47 7.500e-18 143-165 PR00261B 14.12 5.065e-16 65-87 PR00261C 11.37 8.967e-16 143-165 PR00261F 11.57 4.938e-13 143-165 PR00261E 11.08 7.188e-13 65-87 PR00261F 11.57 7.188e-13 65-87 PR00261E 11.08 1.643e-11 143-165
209	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.143e-13 118-173 PF00791C 20.98 7.680e-10 132-171
211	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 5.781e-19 131-158 PR00007B 14.16 4.115e-18 158-178 PR00007C 15.60 1.675e-15 201-223 PR00007D 9.64 7.231e-11 233-244
212	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e-30 43-91
213	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e-30 43-91
215	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 1.900e-29 568-614 BL00039A 18.44 1.871e-23 21-60 BL00039C 15.63 1.720e-11 364-388 BL00039B 19.19 4.064e-11 277-303
217	BL00100	Chloramphenicol acetyltransferase proteins.	BL00100D 17.22 8.484e-09 68-106
219	PR00213	MYELIN P0 PROTEIN SIGNATURE	PR00213C 15.94 3.969e-11 199-227
222	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.947e-09 144-155
224	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.000e-09 901-913
225	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e-19 18-39
226	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.000e-21 21-38 BL00636B 15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	PR00301F 13.98 7.563e-13 329-346 PR00301G 13.78 4.300e-12 361-382
230	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 8.773e-20 35-70 BL00460B 9.73 7.429e-16 78-96 BL00460C 14.35 2.831e-12 111-134 BL00460D 16.89 8.773e-11 140-160
231	PR00647	SENR ORPHAN RECEPTOR SIGNATURE	PR00647B 10.19 8.522e-09 273-287
233	BL00292	Cyclins proteins.	BL00292B 20.31 7.429e-27 244-275 BL00292A 22.87 7.750e-27 201-235
234	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.308e-13 7-29 PR00449C

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e-11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e-10 251-265 PR00019B 11.36 5.320e-09 119-133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e-10 245-259 PR00019B 11.36 5.320e-09 113-127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-10 616-635
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e-12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e-09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e-40 186-239 BL00246E 20.32 1.000e-40 305-351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e-24 70-90 BL00246C 15.56 4.857e-22 150-175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e-10 253-275
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e-09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e-09 61-88
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e-10 421-435
258	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e-18 87-104 PR00094D 12.52 2.731e-14 161-177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e-13 39-54 PR00094E 11.25 7.333e-13 178-193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e-13 60-91
262	BL00388	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e-40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e-21 153-184 BL00388C 18.79 8.147e-16 126-148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e-09 91-101
267	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.529e-09 241-257
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e-37 362-409 BL00226B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			23.86 8.043e-35 196-244 BL00226C 11.23 7.000e-20 261-292 BL00226A 12.77 6.143e-15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.731e-16 235-265 PD02952B 15.57 5.625e-09 215-229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e-40 106-160 PD02929B 18.36 8.800e-17 179-199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e-09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-11 39-59
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e-13 137-184 BL00052B 15.17 5.143e-12 208-235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e-13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e-21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e-21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e-09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e-12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-15 322-339 BL00028 16.07 9.471e-14 433-450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e-13 760-777 BL00028 16.07 9.550e-13 788-805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e-12 461-478 BL00028 16.07 8.435e-12 844-861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e-11 211-228 BL00028 16.07 5.154e-11 732-749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e-11 816-833 BL00028 16.07 7.231e-11 676-693 BL00028 16.07 9.654e-11 564-581

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 4.086e-09 517-534 BL00028 16.07 7.429e-09 489-506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e-16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e-11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e-34 236-269 PF00953A 19.68 5.000e-25 102-129 PF00953B 6.17 1.000e-13 182-194
304	PF00152	tRNA synthetases class II.	PF00152D 21.30 8.364e-28 422-461 PF00152C 28.03 9.250e-21 220-257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e-11 44-67
305	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.250e-35 37-76
306	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e-09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-09 1167-1186
308	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237B 13.03 5.091e-13 188-212 PR00237G 19.63 7.207e-13 268-295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e-10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e-10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e-24 315-339 BL00522F 14.90 1.310e-15 470-494 BL00522A 25.52 1.265e-14 179-226 BL00522E 19.63 8.615e-14 430-460 BL00522B 27.30 9.625e-12 267-313
310	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e-10 856-897
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e-14 151-174 BL00290B 13.17 9.000e-12 211-229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-40 34-85 BL00345A 13.95 9.217e-16 1-20
315	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 5.091e-15 63-76
317	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e-17 79-130
318	BL00216	Sugar transport proteins.	BL00216B 27.64 4.696e-11 164-214
320	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109B 12.27 4.814e-10 216-235

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
321	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.688e-10 329-372
322	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.765e-12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-30 183-236 BL01241 35.81 3.222e-13 282-335
326	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e-12 515-566 BL00412D 16.54 5.705e-11 516-567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e-09 514-565 BL00412D 16.54 1.918e-09 513-564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e-20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e-18 370-418 BL00232B 32.79 5.500e-16 258-306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e-12 256-274 BL00232C 10.65 4.326e-11.368-386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e-11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e-18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e-32 70-115 BL01016E 14.88 5.286e-19 149-177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e-11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e-10 4-19 BL01016F 13.34 1.563e-09 200-212 BL01016B 8.93 8.855e-09 38-50
339	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.500e-11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.231e-33 10-49
341	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e-09 55-109
342	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.400e-30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-40 20-68
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.764e-11 135-154
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e-13 100-116 BL01187B 12.04 8.435e-13 276-292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e-10 54-70 BL01187B 12.04 5.725e-09 231-247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e-11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e-11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e-09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 261-274 PD00066 13.92 6.500e-13 233-246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e-13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e-09 71-126 PF00791B 28.49 7.440e-09 184-239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e-11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e-10 73-95 PR00450C 12.22 3.278e-09 109-131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e-09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e-09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e-09 1038-1092
367	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e-09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e-09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e-15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e-14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e-09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e-12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.757e-34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			10 88-118
380	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 1.000e-23 276-307 BL00107B 13.31 1.692e-12 342-358
381	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 5.714e-12 50-66
382	PR00624	HISTONE H5 SIGNATURE	PR00624D 4.08 4.900e-09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-09 67-80
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e-10 97-130
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e-13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.667e-09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.250e-15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e-11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e-09 272-285 BL00215B 10.44 8.500e-09 165-178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e-16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e-11 141-155
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e-09 55-74
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e-10 118-142
401	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 8.071e-18 331-369 PF00676D 14.40 3.854e-15 486-506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e-28 4432-4469 BL00514G 15.98 6.092e-14 4555-4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e-10 4519-4534 BL00514H 14.95 4.955e-10 4584-4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e-09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e-10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e-09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e-20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e-18 358-406 BL00232B 32.79 5.500e-16 246-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			294 BL00232B 32.79 9.384e-15 463-511 BL00232C 10.65 2.537e-12 244-262 BL00232C 10.65 4.326e-11 356-374 BL00232C 10.65 7.261e-11 461-479 BL00232C 10.65 7.457e-11 27-45
407	PF00426	Outer Capsid protein VP4 (Hemagglutinin).	PF00426B 15.67 5.634e-09 902-940
409	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.695e-09 126-180
410	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 2.731e-09 252-275
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e-09 86-100
412	BL00603	Thymidine kinase cellular-type proteins.	BL00603B 11.39 8.500e-09 542-557
415	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 3.571e-31 245-291 BL00866C 23.26 9.000e-25 331-366
418	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 6.114e-09 590-602
421	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.955e-14 23-78 PF00791B 28.49 3.653e-12 273-328 PF00791B 28.49 4.273e-11 156-211 PF00791B 28.49 7.818e-11 89-144 PF00791B 28.49 1.524e-10 56-111 PF00791C 20.98 3.559e-09 37-76 PF00791C 20.98 5.235e-09 170-209 PF00791C 20.98 5.235e-09 381-420 PF00791B 28.49 6.202e-09 189-244 PF00791B 28.49 7.028e-09 435-490 PF00791B 28.49 8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-28 1645-1679
425	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 5.881e-10 228-251
429	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.600e-11 31-40
431	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 1.844e-34 490-536 BL00039A 18.44 5.615e-19 205-244 BL00039B 19.19 8.920e-16 251-277 BL00039C 15.63 5.781e-15 333-357
432	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 7.652e-12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e-11 195-239 BL00415N 4.29 3.036e-09 809-853
443	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	PR00834F 10.91 6.040e-11 221-234
446	PF01140	Matrix protein (MA),	PF01140D 15.54 9.663e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246-281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PR00568D 13.95 5.551e-09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e-10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e-09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e-25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e-17 230-249 PR00380B 12.64 4.724e-16 194-212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e-24 246-267 PR00253B 13.47 2.000e-23 272-294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e-21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e-09 910-937
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12 33-44
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e-09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e-12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e-09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e-09 393-408
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.900e-38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e-19 451-473 PR00405B 11.83 4.333e-18 430-448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e-10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e-09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e-23 653-673 PR00007A 19.33 6.192e-22 626-653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e-13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e-09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e-12 3-21
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.882e-27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e-09 663-678
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e-17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polyprotein).	15 21-71
498	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e-09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e-11 299-318
501	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 8.579e-12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e-17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e-19 705-722
509	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417B 20.62 2.938e-16 362-395 DM01417D 11.08 3.800e-13 322-338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 346-370
511	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 293-317
512	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 366-390
513	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e-40 110-160 PD01841B 14.35 1.000e-40 181-222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e-40 333-382 PD01841G 24.26 1.000e-40 386-440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e-37 762-804 PD01841E 18.60 3.750e-36 295-333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e-33 490-527 PD01841K 14.81 7.088e-33 924-954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e-21 1054-1073 PD01841I 23.00 2.667e-13 549-591
514	PR00153	CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 7.188e-13 95-111 PR00153E 9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-12 1018-1052
517	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e-09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 8.375e-10 61-95
526	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 3.308e-12 322-343 PF00789C 20.98 5.269e-09 367-392
528	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.500e-16 120-164

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
529	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e-09 60-73
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 123-148
533	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme intermediate proteins.	BL00098C 21.65 2.800e-38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e-35 245-288 BL00098E 22.12 1.000e-34 314-352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e-11 38-50
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370E 11.96 7.429e-22 321-340 PR00370D 16.33 6.143e-21 185-204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e-21 27-46 PR00370C 12.72 3.500e-20 140-157 PR00370A 3.35 6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e-16 285-302 BL00028 16.07 6.294e-14 341-358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e-11 397-414 BL00028 16.07 4.462e-11 453-470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e-10 313-330
537	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 844-881
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 819-856
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e-10 357-375
541	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.000e-40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146
543	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-10 48-65 BL00028 16.07 6.400e-10 193-210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e-09 78-95
545	BL00250	TGF-beta family proteins.	BL00250A 21.24 8.000e-31 293-329 BL00250B 27.37 5.286e-24 354-390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210-227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e-40 8-56 BL01204D 16.42 1.000e-40 177-221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e-22 141-160 BL01204B 15.41 4.333e-16 102-116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e-15 255-276
551	PF00632	HECT-domain (ubiquitin-transferase).	PF00632C 20.66 3.302e-23 1569-1601 PF00632B 18.45 3.700e-21 1515-1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e-14 187-205 BL00290A 20.89 2.059e-14 130-153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e-09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e-09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e-32 118-155
564	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e-10 472-489
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e-15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.977e-13 229-268
569	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199
570	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e-34 454-483 PR00193C 12.60 2.636e-31 223-251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 508-537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e-34 470-499 PR00193C 12.60 2.636e-31 239-267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 524-553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e-10 885-929
576	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e-09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952-965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e-09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 9.000e-11 217-231 PR00019B 11.36 1.350e-09 386-400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e-09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.19 2.125e-25 275-296 PR00253B 13.47 7.923e-24 301-323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e-20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e-11 1233-1252 PR00343C 16.85 5.500e-11 333-352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e-10 1491-1510 PR00343C 16.85 8.230e-10 1686-1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e-37 79-126 DM01537B 21.63 9.491e-30 916-963 DM01537A 15.14 3.186e-11 784-804
586	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e-13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e-13 261-276 BL00478B 14.79 7.709e-09 321-336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e-12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e-16 558-576 PR00205A 14.73 9.300e-13 542-558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e-10 336-354
596	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.789e-18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e-10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e-27 985-1014 BL00242C 16.86 4.115e-26 286-316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e-12 189-199 BL00242D 13.57 3.455e-11 421-446 BL00242A 13.80

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			5.000e-11 61-73 BL00242D 13.57 4.986e-10 291-316
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e-09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e-10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e-12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e-09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e-10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e-13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-15 211-228
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.411e-10 877-897 DM01206B 10.69 8.027e-10 861-881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10:69 1.456e-09 859-879 DM01206B 10.69 1.797e-09 879-899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e-09 898-918 DM01206B 10.69 7.949e-09 871-891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e-28 129-158 PD02699C 24.84 1.000e-27 317-364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 5.143e-12 531-551 DM01206B 10.69 2.603e-10 535-555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e-21 561-582
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e-10 647-692 BL00239C 18.75 8.304e-10 543-566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e-09 326-339
624	BL00641	Respiratory-chain NADH dehydrogenase 75 Kd	BL00641C 21.10 1.000e-40 157-202 BL00641E

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		subunit proteins.	24.37 1.000e-40 255-308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e-37 48-80 BL00641B 12.62 5.846e-34 113-139 BL00641D 13.23 9.308e-29 216-240
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e-18 367-380 PR00103B 13.39 2.080e-14 297-312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e-12 346-358 PR00103C 15.68 1.000e-11 334-344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e-10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 6.211e-16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.500e-14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e-10 1324-1344 DM01206B 10.69 4.822e-10 1276-1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e-10 1280-1300 DM01206B 10.69 4.532e-09 1320-1340 DM01206B 10.69 7.266e-09 1326-1346
635	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.600e-23 145-176 BL00107B 13.31 2.636e-13 211-227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e-30 101-143 BL00657B 22.27 7.750e-26 149-192
637	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e-13 385-400 PF00628 15.84 3.455e-12 464-479
648	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 4.000e-25 332-357 BL01129C 25.56 8.200e-23 236-279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e-10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e-13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e-12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e-24 253-274 PR00253C 13.85 8.800e-24 313-335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e-11 969-997 PD01719A 12.89 3.961e-10 128-156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e-09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 8.397e-09 563-578
658	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 8.397e-09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e-13 539-572 DM00215 19.43 4.750e-12 549-582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e-10 548-581 DM00215 19.43 4.054e-10 550-583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e-10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e-09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e-23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
666	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e-10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e-16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e-09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e-09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e-34 356-410 PD00131C 19.59 1.346e-26 504-542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e-10 106-123
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e-13 593-608 PR00320B 12.19 4.115e-12 635-650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e-10 635-650 PR00320C 13.01 6.400e-10 593-608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e-13 572-587 PR00320B 12.19 4.115e-12 614-629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e-10 614-629 PR00320C 13.01 6.400e-10 572-587 PR00320B 12.19 3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e-09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 3.700e-16 225-236 PF00642 11.59 7.900e-12 187-198
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e-10 286-296
681	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 4.200e-19 227-257
682	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 4.000e-09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.500e-10 538-553
689	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.	BL01024A 10.26 1.000e-40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e-40 146-185 BL01024D 13.22 1.000e-40 185-222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e-40 266-317 BL01024G 11.09 1.000e-40 317-349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e-31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e-09 45-57
693	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e-09 45-57
694	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e-09 58-70
696	BL00680	Methionine aminopeptidase subfamily 1 proteins.	BL00680 14.37 5.304e-17 173-195
697	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 3.418e-11 242-265
698	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930E 15.41 1.367e-37 170-215 DM01930F 14.16 8.232e-28 267-303 DM01930B 19.86 9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	PR00869A 12.80 1.281e-16 245-263
701	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.174e-10 77-91 PR00048A 10.52 6.870e-10 133-147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e-09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e-25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e-15 86-98 BL00523C 12.64 5.500e-13 137-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e-10 513-523 BL00523F 10.85 6.351e-09 413-424
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e-12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e-09 364-374
707	PD00787	SYNTHASE BIOSYNTHESIS TRANSFERASE.	PD00787A 14.84 8.941e-14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e-10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354V 10.69 4.977e-38 425-465 DM01354X 13.86 7.300e-34 376-415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e-10 356-376
713	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.545e-27 450-496 BL00039A 18.44 2.537e-18 147-186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e-13 194-220
715	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 4.981e-10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e-21 106-161
718	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e-12 131-142
719	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243B 17.54 1.000e-40 131-172 BL00243C 16.42 1.000e-40 172-208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e-40 314-358 BL00243I 31.77 6.571e-39 607-650 BL00243E 16.70 3.077e-35 274-304 BL00243G 21.38 3.625e-34 358-400 BL00243H 17.53 5.235e-29 567-593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e-16 477-503 BL00243H 17.53 2.304e-11 524-550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e-09 610-653
720	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 8.022e-09 20-36
722	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704D 11.05 5.905e-34 135-161 PR00704F 13.61 7.000e-26 190-218 PR00704E 12.55 8.071e-26 165-189

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00704B 17.94 2.241e-23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e-18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.125e-13 277-292 PR00320A 16.74 1.310e-11 277-292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e-11 323-338 PR00320B 12.19 4.343e-10 323-338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e-16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.89 9.082e-10 787-798
738	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039A 18.44 2.565e-28 26-65 BL00039D 21.67 2.105e-20 338-384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e-11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e-31 326-353 BL01289B 10.45 9.571e-17 353-383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.079e-12 41-81
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e-40 256-305 BL00965B 17.77 1.600e-25 126-153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e-25 231-273 BL00021B 13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e-11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e-10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e-11 384-429 BL00795C 17.06 9.444e-11 370-415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e-16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e-09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e-12 99-150
762	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e-10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e-29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.061e-10 309-324 BL01208B 15.83 8.031e-10 165-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones receptors DNA-binding region proteins.	BL00031A 19.55 9.571e-32 208-241 BL00031B 22.25 5.500e-27 242-274
772	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.450e-18 4-26 PR00449E 13.50 3.520e-14 142-165 PR00449C 17.27 3.032e-13 44-67 PR00449D 10.79 8.579e-13 107-121 PR00449B 14.34 3.455e-11 27-44
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-23 299-329 BL00523A 13.36 2.200e-13 47-64 BL00523B 8.64 2.607e-13 91-103 BL00523D 9.89 7.923e-12 224-236 BL00523C 12.64 4.512e-10 141-152 BL00523F 10.85 5.821e-10 373-384
775	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 568-585
776	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 621-638
777	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 595-612
778	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 8.412e-11 322-341 BL00030A 14.39 7.000e-10 220-239
779	PR00079	GLUCOSE-6-PHOSPHATE DEHYDROGENASE SIGNATURE	PR00079B 12.98 2.929e-26 193-222 PR00079E 16.65 4.150e-23 348-375 PR00079C 8.68 6.351e-16 246-264 PR00079D 13.51 7.070e-16 264-281 PR00079A 16.12 6.769e-13 169-183
781	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.250e-17 10-35 BL00215A 15.82 6.000e-16 221-246 BL00215A 15.82 7.857e-12 108-133 BL00215B 10.44 9.526e-11 168-181
783	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 6.276e-09 159-173
785	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.	BL00690B 13.38 1.000e-12 147-165 BL00690A 6.87 5.320e-10 114-124 BL00690C 7.51 3.189e-09 218-228
786	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 8.500e-16 50-73 PR00449A 13.20 5.235e-14 8-30 PR00449E 13.50 2.853e-11 150-173 PR00449D 10.79 1.545e-09 111-125
788	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.767e-10 1-21
790	BL00915	Phosphatidylinositol 3- and 4-kinases proteins.	BL00915C 22.43 9.182e-39 725-764 BL00915B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			22.78 5.050e-33 633-671 BL00915D 27.02 1.529e-21 795-831 BL00915A 10.09 1.000e-13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 6.294e-10 120-138 PR00208A 12.59 6.294e-10 121-139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e-10 123-141 PR00208A 12.59 6.294e-10 124-142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e-10 126-144 PR00208A 12.59 6.294e-10 127-145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e-10 129-147 PR00208A 12.59 7.411e-09 130-148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e-09 132-150 PR00208A 12.59 8.274e-09 118-136 PR00208A 12.59 8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-16 302-320 PR00205A 14.73 1.257e-11 284-300 PR00205C 13.65 1.333e-11 337-352
796	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e-12 196-247 BL00412D 16.54 5.705e-11 197-248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e-09 195-246 BL00412D 16.54 1.918e-09 194-245 BL00412D 16.54 2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.319e-13 40-58
799	BL01052	Calponin family repeat proteins.	BL01052C 18.51 1.000e-40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e-25 52-78 BL01052D 10.26 5.737e-25 174-194
800	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 3.714e-09 197-240
801	BL00309	Vertebrate galactoside-binding lectin proteins.	BL00309C 18.65 1.621e-09 62-87
802	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245D 10.47 5.224e-09 187-199
804	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774A 16.47 8.457e-10 110-156
808	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667C 11.71 9.875e-09 12-28
810	PD02346	PHOTOSYSTEM II PROTEIN PRECURSOR	PD02346F 12.89 4.340e-09 317-354

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit proteins.	BL00685B 14.41 6.779e-14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 9.419e-10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17 22-65
815	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.923e-15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e-14 18-31 PD00066 13.92 7.000e-13 130-143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e-13 102-115 PD00066 13.92 4.429e-12 186-199 PD00066 13.92 1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase proteins.	BL01195C 20.12 3.348e-20 100-139
820	BL00520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e-09 1-14
822	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 8.113e-09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 2.268e-10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732e-28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 7.000e-21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e-13 25-45
831	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e-09 47-61 PR00019B 11.36 1.720e-09 136-150 PR00019B 11.36 3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.438e-16 164-183 PR00011D 14.03 6.850e-16 164-183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e-12 231-260 PR00011D 14.03 9.852e-11 212-231
834	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e-12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 4.000e-10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e-12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-09 78-111
839	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 8.302e-09 73-116
840	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 5.091e-22 369-390 PR00700D 12.47 5.765e-21 491-510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			11 538-549 PR00700E 17.57 3.100e-10 522-538
841	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e-13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e-40 58-112 PD02785A 15.23 1.955e-28 8-57
845	BL00826	MARCKS family proteins.	BL00826C 7.63 6.738e-09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e-10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e-08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e-09 12-27
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e-16 246-280
852	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e-40 723-778 BL00420B 22.67 1.321e-38 933-988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 587-642 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 808-819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1018-1029 BL00420C 11.90 7.955e-10 567-578
853	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e-40 756-811 BL00420B 22.67 1.321e-38 966-1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 620-675 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 841-852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1051-1062 BL00420C 11.90

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 2.778e-09 64-83
859	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e-13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e-10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e-17 23-41 PR00988C 13.64 8.714e-16 107-123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e-10 60-72
863	BL00215	Mitochondrial energy transfer proteins.	BL00215B 10.44 8.071e-12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e-24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e-17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e-17 153-171 PR00775G 10.64 6.850e-15 267-286 PR00775F 12.76 6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e-09 89-121
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.596e-29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e-26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e-10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-40 30-85
874	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e-32 665-711
876	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 298-315
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 4.176e-10 97-141
879	BL01189	Ribosomal protein S12e proteins.	BL01189A 14.27 1.000e-40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e-25 62-104 BL00284B 17.99 6.182e-12 35-56
889	BL00216	Sugar transport proteins.	BL00216B 27.64 4.375e-21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE	PR00391E 12.50 7.785e-15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e-13 191-207 PR00391A 7.83 5.390e-11 16-36
897	PR00327	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.800e-26 386-432 BL00039A 18.44 6.674e-16 113-152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 254-267 PD00066 13.92 8.200e-16 282-295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e-16 366-379 PD00066 13.92 8.200e-16 394-407 PD00066 13.92 8.200e-14 338-351
902	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 9.321e-11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e-09 97-111
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PR00381E 8.75 6.586e-25 335-356 PR00381B 18.17 2.667e-24 204-224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e-24 226-245 PR00381D 13.94 1.084e-22 291-309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e-13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e-11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e-09 333-351 PR00381C 12.48 7.120e-09 310-329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e-09 525-549
907	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e-09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.800e-30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e-09 364-392
922	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09 500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e-09 323-338 PR00320C 13.01 5.500e-09 187-202
924	PD02181	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	PD02181D 12.85 8.609e-09 36-64
926	BL00019	Actinin-type actin-binding domain proteins.	BL00019C 14.66 7.453e-25 108-144 BL00019B 13.34 6.510e-11 61-84 BL00019D 15.33 9.338e-11 205-235 BL00019A 12.56 2.373e-10 34-45
928	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325 BL00678 9.67 7.600e-10 360-371 BL00678 9.67 8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.857e-10 137-146
930	BL01085	Ribulose-phosphate 3-epimerase family proteins.	BL01085D 16.55 4.600e-24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-epimerase family proteins.	BL01085D 16.55 4.600e-24 152-183 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e-09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE	PR00862D 16.17 4.086e-09 63-84
945	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e-09 407-420
948	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 7.429e-18 52-68 BL00479A 19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09 100-111
954	PD01311	PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.	PD01311A 30.23 5.909e-10 66-111
955	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-12 47-60
956	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-12 47-60
957	BL00379	CDP-alcohol phosphatidyltransferases proteins.	BL00379 24.64 1.610e-15 111-148
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e-10 31-75
960	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e-14 110-154
962	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.586e-13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-11 210-225
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e-09 55-70
967	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 1.286e-12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e-10 73-93 DM01206B 10.69 3.962e-09 108-128 DM01206B 10.69 5.671e-09 38-58
969	PF01008	Initiation factor 2 subunit.	PF01008B 25.59 4.724e-31 417-460 PF01008C 12.25 5.333e-18 506-526 PF01008A 20.14 5.875e-15 369-390

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e-10 112-143 BL01277A 17.39 9.806e-10 40-78
975	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.605e-12 130-145 BL01159 13.85 4.122e-10 171-186
977	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e-09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e-19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e-13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e-36 169-199 PR00312I 15.78 5.286e-35 332-361 PR00312F 15.06 5.865e-35 199-229 PR00312N 13.31 8.313e-35 263-291 PR00312J 13.73 5.688e-34 363-392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e-33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e-32 230-258 PR00312A 11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e-09 414-449
982	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e-09 127-149
983	BL01150	Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e-40 156-202 BL01150A 14.10 8.200e-39 100-138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e-14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e-10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e-10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e-09 3-48
987	BL00939	Ribosomal protein L1e proteins.	BL00939F 17.27 5.393e-09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e-25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e-11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e-24 73-94 PR00926D 10.53 3.250e-23 126-145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.000e-15 11-25 PR00926F 17.75 5.565e-09 120-143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e-40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e-40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e-29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e-40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e-35 248-298 BL00406A 9.95 3.348e-29 11-46
1007	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304D 11.04 8.714e-22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e-19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e-13 418-431
1009	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.929e-32 9-48
1011	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.929e-32 68-107
1012	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e-10 64-73
1016	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168H 12.08 1.000e-11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 1.391e-32 261-302 PD00930A 25.62 9.550e-22 157-183
1022	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175A 15.42 5.179e-12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305D 16.34 1.439e-10 158-185
1026	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.436e-18 238-288 BL00353C 14.83 8.844e-11 288-335
1028	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.310e-33 43-91
1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e-09 111-133
1034	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 3.429e-09 154-171
1037	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.657e-09 5-44
1038	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 4.259e-11 55-82
1039	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.036e-09 17-69
1040	PR00970	ARGININE ADP-RIBOSYLTRANSFERASE	PR00970A 17.73 6.143e-20 56-78 PR00970D

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e-16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e-13 86-105 PR00970C 11.05 1.643e-11 115-130 PR00970E 11.23 9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.786e-13 114-128 PR00048A 10.52 1.000e-09 172-186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e-11 218-236 BL00615B 12.25 1.857e-10 317-331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e-10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases family proteins.	BL01216D 21.75 4.316e-28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e-12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e-40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e-31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.238e-11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e-23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e-11 118-152
1060	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.455e-35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e-13 280-296
1065	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e-09 115-129 PR00019B 11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.600e-16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e-14 172-191 PR00326D 19.09 1.257e-13 217-236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.518e-11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e-09 350-387
1075	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e-20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e-11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e-08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e-12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e-10 23-57
1094	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e-18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e-12 162-182 BL00460C 14.35 5.500e-09 133-156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e-22 67-105 PD02811B 17.07 2.263e-21 110-151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e-22 60-98 PD02811B 17.07 2.263e-21 111-144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e-09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-13 111-147
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e-10 15-37 PR00449E 13.50 1.857e-09 185-208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e-20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e-10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 4.857e-10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e-12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e-09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis-trans isomerase signatur.	BL00170C 18.49 3.077e-33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e-15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e-15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e-38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e-27 157-187 BL00990D 16.13 5.320e-18 403-422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e-34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			32 159-188 PR00314A 14.53 1.281e-22 13-34
1139	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 6.364e-13 13-57
1141	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.000e-19 451-482 BL00107B 13.31 3.077e-12 519-535
1148	PR00685	TRANSCRIPTION INITIATION FACTOR IIB SIGNATURE	PR00685A 13.62 4.676e-09 21-42
1155	PD01652	RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB.	PD01652B 8.50 9.396e-10 522-574 PD01652B 8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e-28 81-127 PD02894B 13.93 1.188e-27 178-211
1159	BL00623	GMC oxidoreductases proteins.	BL00623E 15.00 3.531e-20 391-414 BL00623C 10.86 4.240e-20 155-176
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.	PD01937A 6.68 3.475e-09 330-341
1162	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.	PD01937A 6.68 3.475e-09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-10 214-239 PR00624D 11.94 1.961e-09 312-337
1167	BL00226	Intermediate filaments proteins.	BL00226B 23.86 7.384e-09 302-350
1177	BL01032	Protein phosphatase 2C proteins.	BL01032D 8.33 1.422e-10 34-48
1178	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 1.794e-10 205-220 PR00320C 13.01 7.840e-10 205-220 PR00320B 12.19 8.457e-10 35-50 PR00320A 16.74 7.146e-09 35-50 PR00320B 12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-19 765-784
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e-11 152-187
1184	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 4.103e-18 1089-1113
1185	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.553e-13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e-11 104-129
1187	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 2.761e-10 77-93
1188	BL00878	Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.	BL00878B 10.95 6.000e-16 189-204 BL00878C 17.74 8.435e-15 225-245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e-09 270-289
1191	PD02939	PROTEIN GLUTATHIONE SYNTHETASE SY.	PD02939B 10.10 2.723e-12 203-220 PD02939C 20.01 1.000e-11 224-252
1193	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-28 72-101 PR00345E

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e-28 101-125 PR00345D 10.97 1.964e-24 125-149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e-28 137-161 PR00345D 10.97 1.964e-24 161-185 PR00345A 13.46 5.645e-16 79-98
1195	PF00995	Sec1 family.	PF00995B 17.37 1.120e-13 224-264
1196	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 6.738e-11 15-47
1197	BL01298	Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959e-09 51-73
1203	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 1.000e-14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PR00118F 16.42 9.386e-09 213-229
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e-37 184-229 BL01183D 27.71 8.535e-27 264-307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e-09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e-09 105-146
1209	PF00023	Ank repeat proteins.	PF00023A 16.03 4.857e-11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e-14 227-241 PR00048A 10.52 4.316e-11 199-213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e-10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e-09 44-64
1216	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e-10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.348e-11 249-264
1222	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e-15 295-308 PD00066 13.92 7.231e-15 406-419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e-12 434-447 PD00066 13.92 3.348e-11 350-363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e-40 13-61
1226	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.439e-09 279-330
1227	BL00437	Catalase proximal heme-ligand proteins.	BL00437A 18.82 1.000e-40 49-101 BL00437B 16.28 1.000e-40 114-168 BL00437C 21.86

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			1.000e-40 190-219 BL00437D 25.72 1.000e-40 248-301 BL00437E 23.95 1.000e-40 327-379
1230	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e-10 6-60
1231	PR00735	GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE	PR00735A 11.19 6.857e-09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e-10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e-10 158-176
1235	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 2.778e-09 75-121
1237	BL00027	'Homeobox' domain proteins.	BL00027 26.43 1.818e-21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-11 10-25
1246	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168L 9.47 2.837e-10 31-46 PD01168L 9.47 4.490e-10 174-189 PD01168L 9.47 7.612e-10 183-198
1249	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10 183-196
1254	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 2.440e-36 96-144
1255	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-11 8-52
1256	BL00373	Phosphoribosylglycinamide formyltransferase proteins.	BL00373C 10.35 3.348e-12 143-156
1258	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.217e-10 174-193
1259	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.286e-10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE SIGNATURE	PR00070D 11.63 1.000e-15 112-127 PR00070C 13.09 9.500e-15 51-63 PR00070A 12.92 5.500e-12 16-27
1262	BL00462	Gamma-glutamyltranspeptidase proteins.	BL00462A 20.89 6.438e-24 140-183 BL00462B 17.88 5.500e-20 230-267 BL00462C 27.41 2.023e-11 292-347
1263	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 9.455e-11 62-83
1264	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-11 17-61
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.714e-18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e-12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 9.308e-22 40-63 PR00449E 13.50 1.000e-16 137-160 PR00449D 10.79 3.520e-11 102-116
1270	BL00276	Channel forming colicins proteins.	BL00276A 8.87 1.500e-09 17-29
1275	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOOLO.	PD02327C 15.47 9.769e-09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165-179 PR00412A 13.23 3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e-10 127-157
1279	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e-13 128-145
1280	BL01220	Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e-15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e-10 33-42
1287	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e-11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802B 16.51 1.610e-10 81-105
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e-09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e-14 268-283
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e-28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637E 11.27 4.250e-09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e-17 13-38 BL00215A 15.82 1.000e-16 226-251 BL00215A 15.82 2.658e-13 107-132
1308	PR00898	VASOPRESSIN V2 RECEPTOR SIGNATURE	PR00898H 11.34 4.682e-09 552-572
1309	PD000301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD000301B 5.49 2.731e-09 390-401
1310	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.654e-13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family proteins.	BL00194 12.16 1.900e-11 15-28
1314	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 8.969e-10 53-97
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e-13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e-24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e-12 74-86
1327	PF00514	Armadillo/beta-catenin-like repeat proteins.	PF00514A 31.30 7.268e-11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e-11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 7.239e-09 25-43
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	PR00161C 9.51 4.930e-09 317-337
1333	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.769e-33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e-09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e-13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e-16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e-21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e-09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e-10 135-146
1348	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 7.231e-13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e-32 416-445 PR00193C 12.60 6.318e-31 179-207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e-22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PR00447E 9.73 1.554e-15 299-319 PR00447D 13.54 3.408e-15 200-224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-10 353-373
1353	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 6.667e-26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.950e-29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e-18 225-249 BL00039B 19.19 3.182e-14 141-167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e-12 84-101 PF00615C 10.06 8.412e-12 162-176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.234e-29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e-18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e-12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e-30 136-171 BL01272C 11.68 3.314e-25 249-274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e-30 113-148 BL01272C 11.68 3.314e-25 226-251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e-09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e-09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			10 1-19
1371	BL00242	Integrins alpha chain proteins.	BL00242B 8.13 8.615e-09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 7.353e-19 46-67 PR00625A 12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 3.778e-09 90-130
1374	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962C 8.00 6.337e-09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR-ASSOCIATE.	PD02475A 23.18 8.552e-10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.571e-32 24-63
1380	BL00194	Thioredoxin family proteins.	BL00194 12.16 8.333e-12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 1.458e-15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 243-254
1384	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 271-282
1385	BL00303	S-100/1CaBP type calcium binding protein.	BL00303B 26.15 6.203e-10 95-132
1386	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e-09 1574-1628
1387	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e-11 52-61
1389	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.600e-30 10-49
1390	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.512e-31 32-71
1392	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.723e-10 127-137
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.625e-25 88-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e-16 208-226 PR00380C 13:18 6.538e-16 243-262
1394	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e-14 462-475 PD00066 13.92 8.800e-14 348-361 PD00066 13:92 9.571e-12 405-418 PD00066 13.92 6.087e-11 490-503 PD00066 13.92 8.043e-11 320-333
1398	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.786e-32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.038e-09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 7.324e-15 363-389
1407	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e-10 457-476
1408	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.550e-11 179-193 PR00019A 11.19 8.826e-10 228-242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.196e-12 182-202 PR00510B 12.96 8.767e-12 210-230 PR00510F 9.88 8.172e-10 58-75 PR00510D 9.21 2.367e-09 251-267
1410	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.696e-09 31-44
1412	BL00358	Ribosomal protein L5 proteins.	BL00358B 22.76 1.000e-40 57-103 BL00358C 13.75 6.087e-14 122-136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e-11 33-44
1414	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 7.338e-10 511-534
1415	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 4.300e-29 40-77
1417	PR00681	RIBOSOMAL PROTEIN S1 SIGNATURE	PR00681G 12.54 2.149e-09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.462e-09 171-208
1419	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 1.571e-09 428-443
1420	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941A 14.81 1.000e-40 142-196 PD01941B 15.02 7.049e-30 400-447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e-19 488-543 PD01941D 27.18 9.614e-18 641-690 PD01941F 28.52 5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-12 199-217
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e-11 1009-1028
1424	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 8.200e-14 307-306 BL50002A 14.19 9.250e-12 298-317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e-12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e-12 377-392
1427	PR00405	HIV REV INTERACTING PROTRIN SIGNATURE	PR00405B 11.83 5.114e-16 281-299 PR00405A 17.71 4.306e-14 262-282
1428	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.219e-34 147-193
1429	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.920e-10 577-592
1430	PR00378	INOSITOL PHOSPHATASE SIGNATURE	PR00378D 16.66 7.563e-12 295-314 PR00378B 13.80 8.650e-10 166-186
1431	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PROTEIN SIGNATURE	10 103-124
1433	BL01113	C1q domain proteins.	BL01113B 18.26 7.049e-15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e-10 135-150
1436	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.000e-12 84-103
1438	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.500e-09 250-268 BL00290A 20.89 4.000e-09 188-211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e-08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e-40 73-123 PD01841B 14.35 1.000e-40 144-185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e-40 296-345 PD01841G 24.26 1.000e-40 349-403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e-40 895-932 PD01841L 18.42 1.000e-40 1083-1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e-35 1041-1071 PD01841H 21.30 3.189e-31 435-472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-20 1175-1194
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e-09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.080e-09 402-416
1448	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315D 18.40 7.393e-09 23-67
1451	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 2.800e-10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e-09 382-405
1455	PF00777	Sialyltransferase family.	PF00777C 18.60 2.929e-22 4-59
1457	BL00927	Trehalase proteins.	BL00927C 10.83 8.085e-09 42-53
1460	BL00545	Aldose 1-epimerase proteins.	BL00545C 11.28 7.353e-17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e-09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e-09 233-245
1472	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129B 13.25 5.250e-22 170-195 BL01129C 25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e-09 2114-2145
1475	PF00686	Starch binding domain proteins.	PF00686A 13.45 9.100e-09 267-277

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e-10 466-476
1478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e-10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10 292-305
1480	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385e-15 69-87 BL00290A 20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150P 10.45 9.039e-09 21-51
1482	PF00780	Domain found in NIK1-like kinases, mouse citron and yeast ROM.	PF00780I 14.69 4.825e-09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e-09 108-162
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.909e-25 17-56
1486	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.529e-09 34-50
1488	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 9.586e-10 116-162
1490	BL00166	Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e-24 190-226 BL00166C 18.93 5.500e-14 140-167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases proteins.	BL00452D 28.59 3.700e-31 63-106 BL00452E 11.92 3.045e-13 115-131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.667e-09 532-546
1497	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-11 384-400 BL00107A 18.39 5.345e-11 322-353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-24 112-155
1503	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 5.800e-24 448-475 BL01177C 17.39 5.333e-19 402-421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e-15 427-445
1506	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e-14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e-10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e-22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e-09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e-14 168-218
1518	BL00600	Aminotransferases class-III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.141e-19 98-122 BL00600E 16.43 1.771e-17 302-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			331 BL00600G 12.43 9.625e-17 377-396 BL00600B 19.60 5.091e-15 160-186 BL00600C 16.18 6.040e-12 190-206 BL00600F 8.77 1.000e-11 343-356 BL00600D 8.71 1.000e-10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 9.600e-18 41-82
1528	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 4.774e-11 192-207 PR00320B 12.19 8.839e-11 272-287 PR00320B 12.19 9.743e-10 106-121 PR00320A 16.74 1.878e-09 192-207 PR00320A 16.74 2.317e-09 106-121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e-09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 4.508e-15 171-184
1539	PF00781	Diacylglycerol kinase catalytic domain proteins (presumed).	PF00781D 11.11 7.593e-10 103-127
1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e-29 312-334 PR00965E 12.93 5.846e-29 172-195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e-27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e-27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e-25 35-55 PR00965I 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.719e-17 163-207
1543	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e-40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e-21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.857e-10 182-197 PR00049D 0.00 7.102e-09 67-82
1547	BL00951	BR lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e-40 93-142 BL00951D 13.94 8.714e-40 142-177 BL00951A 15.10 1.000e-38 2-38 BL00951B 14.23 6.250e-33 38-69
1548	BL00536	Ubiquitin-activating enzyme proteins.	BL00536F 13.65 8.920e-30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e-18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	PR00139C 11.72 9.679e-09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e-09 58-73

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1556	BL00061	Short-chain dehydrogenases/reductase family proteins.	BL00061B 25.79 6.276e-13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1562	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 6.600e-18 412-436 BL00522B 27.30 1.738e-16 364-410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e-14 502-532 BL00522F 14.90 2.385e-13 551-575
1563	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 1.947e-11 46-59
1564	BL00299	Ubiquitin domain proteins.	BL00299 28.84 2.823e-10 324-376
1566	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.594e-17 184-228 BL01013C 9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306
1570	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e-17 297-313 BL00479A 19.86 6.625e-15 271-294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e-12 173-189
1576	PR00665	OXYTOCIN RECEPTOR SIGNATURE	PR00665G 12.36 4.673e-24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e-22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e-19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e-15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e-10 127-137
1579	BL00524	Somatomedin B domain proteins.	BL00524A 9.65 6.776e-14 52-73
1580	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894B 13.93 6.959e-16 182-215 PD02894A 21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 5.292e-12 32-54 BL00411H 15.66 4.441e-11 245-276
1582	PR00604	CLASS IA AND IB CYTOCHROME C SIGNATURE	PR00604A 11.13 2.440e-09 79-87
1584	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 1.000e-10 225-238
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e-11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354B 11.61 7.750e-09 474-495

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e-33 180-210 PR00072A 12.75 6.040e-25 120-145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e-22 276-295 PR00072E 10.54 1.360e-19 301-316 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e-15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e-22 61-113 BL00191K 17.38 9.027e-12 398-442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e-13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e-16 1175-1193 DM00517A 8.21 1.000e-11 1015-1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e-27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e-12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e-10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e-09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e-11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e-09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e-10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e-10 136-187
1605	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.571e-10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e-23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e-08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e-10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e-09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e-09 932-983 BL00412D 16.54 7.153e-09 933-984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.531e-25 54-83 BL00559K 13.17 2.957e-18 197-224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e-16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e-22 500-541 PD01427A 19.94 8.773e-18 439-472

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1616	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.485e-09 152-201 BL00115Z 3.12 9.603e-09 145-194
1617	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 7.750e-32 51-88 BL00303A 21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 16.02 8.754e-09 137-147
1619	PD01888	PEPTIDE REDUCTASE PROTEIN METHI.	PD01888B 25.10 1.000e-40 47-97 PD01888C 21.56 7.000e-30 125-155 PD01888A 12.84 8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 3.455e-09 692-704 PR00239E 1.58 4.580e-09 697-709 PR00239E 1.58 4.580e-09 702-714 PR00239E 1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860B 7.04 1.900e-18 27-41 PR00860C 9.61 1.474e-14 41-51 PR00860A 5.46 1.720e-14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 8.027e-11 77-95
1626	BL00325	Actin-depolymerizing proteins.	BL00325B 21.66 1.000e-40 93-139 BL00325A 24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase proteins.	BL00064B 23.57 1.000e-40 82-130 BL00064C 17.28 1.000e-40 137-182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.882e-36 286-331 BL00064A 21.16 1.000e-33 22-60 BL00064D 14.19 6.500e-31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27 SIGNATURE	PR00063B 15.24 9.700e-11 59-84 PR00063A 11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239D 0.00 1.105e-11 36-49 PR00239C 3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-10 133-183
1637	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 5.388e-11 11-43
1639	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 8.144e-12 132-177
1640	PR00015	GRAM-POSITIVE COCCUS SURFACE PROTEIN ANCHOR SIGNATURE	PR00015B 9.84 8.468e-10 128-149
1641	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 5.935e-11 364-379 PR00320A 16.74 7.828e-11 364-379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e-10 364-379 PR00320B 12.19 5.114e-10 279-294 PR00320A 16.74 1.659e-09 279-294

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e-09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e-09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e-11 74-94
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e-17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.270e-21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e-16 332-351 PR00380B 12.64 6.657e-15 292-310
1647	DM01242	3 THREONINE--TRNA LIGASE.	DM01242C 17.15 9.791e-37 340-381 DM01242E 23.00 5.071e-31 463-505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e-18 265-314 DM01242F 10.61 7.618e-14 526-540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e-10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e-11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e-12 11-35 BL00933E 13.80 9.217e-09 456-472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e-10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e-17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e-17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e-16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.939e-11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e-10 442-455
1659	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e-12 376-401 BL00972E 20.72 5.629e-09 446-468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e-15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e-13 1140-1157 PR00105B 12.32 2.800e-12 1259-1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e-33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e-19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10 489-502
1667	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.500e-38 7-46
1669	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 1.188e-17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e-10 13-37
1671	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 3.100e-10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e-20 27-49
1673	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.329e-09 686-707
1674	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.580e-11 343-358 PR00049D 0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e-19 427-448 PR00747G 14.50 2.286e-18 368-393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747D 15.23 8.759e-17 163-183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 311-328
1677	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e-19 309-330 PR00747G 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-210
1680	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331
1681	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.346e-13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR SIGNATURE	PR00646H 6.32 4.188e-09 755-771
1690	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e-09 75-129
1691	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456B 3.06 7.281e-10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456B 3.06 8.125e-10 420-435
1692	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e-10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456B 3.06 8.125e-10 489-504
1693	BL00674	AAA-protein family proteins.	BL00674C 22.60 8.043e-24 274-317 BL00674B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			4.46 4.000e-23 241-263 BL00674D 23.41 8.560e-18 338-385 BL00674E 15.24 1.720e-15 414-434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e-10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e-13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e-09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e-12 283-300 BL00028 16.07 3.769e-11 255-272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e-11 227-244 BL00028 16.07 1.600e-10 199-216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e-15 62-102 BL01019B 19.49 4.000e-15 107-162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.484e-12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e-14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e-10 116-130 PR00019B 11.36 4.600e-09 113-127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e-11 232-247 BL01159 13.85 5.408e-10 613-628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.050e-10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e-11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e-11 230-241
1715	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 7.129e-09 7-51
1718	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e-10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e-09 432-483
1721	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 8.448e-12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e-09 418-428
1724	BL01279	Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa.	BL01279A 24.27 5.663e-12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170
1730	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 1.089e-09 17-61

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-10 316-370
1733	PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e-22 246-279 PF00850D 14.76 6.850e-20 177-201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e-14 281-323
1734	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 5.932e-09 292-307
1735	DM00179	W KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e-10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e-15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e-11 45-57 PR00081E 17.54 3.935e-10 150-168
1747	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439H 18.24 8.435e-14 65-91 BL00439G 13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 7.158e-11 4-20
1751	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e-14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e-13 61-74 PD00066 13.92 6.571e-12 117-130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e-18 33-77
1754	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e-09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e-09 287-318
1756	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.750e-35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e-09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e-11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e-14 523-539
1776	BL00942	glpT family of transporters proteins.	BL00942F 15.07 4.343e-10 371-389 BL00942B 20.36 8.040e-09 94-137
1777	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e-20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e-11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e-18 611-655 BL01013A 25.14 2.881e-15 344-380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e-12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e-13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e-13 492-515

* results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.1(%CRU01!.DOC)

TABLE 4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP_GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	1.6e-119	410.5
21	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	4.3e-102	352.6
22	pkinase	Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	0	1077.7
26	C1q	C1q domain	1.9e-10	44.4
27	Ribosomal_L23	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L23	Ribosomal protein L23	1e-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Ets-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
52	ras	Ras family	8.5e-45	162.3
53	PRK	Phosphoribulokinase	2.1e-65	230.7
54	myb_DNA-binding	Myb-like DNA-binding domain	0.096	15.2
55	voltage_CLC	Voltage gated chloride channels	3.3e-186	631.9
56	sugar_tr	Sugar (and other) transporter	0.00015	-84.3
57	TBC	TBC domain	2.2e-37	137.6
58	ank	Ank repeat	5.9e-25	96.3
59	ank	Ank repeat	5.9e-25	96.3
67	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	7.9e-49	175.6
68	C2	C2 domain	7.9e-54	192.2
69	C2	C2 domain	2.3e-54	194.0
70	Kelch	Kelch motif	9.4e-99	341.5
72	ig	Immunoglobulin domain	8.2e-28	94.7
73	pkinase	Eukaryotic protein kinase	8e-69	242.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		domain		
74	pkinase	Eukaryotic protein kinase domain	2.8e-38	140.6
76	zf-C4_Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin_G	Laminin G domain	6.1e-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductase	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C	Protein phosphatase 2C	2.2e-71	250.6
129	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	3.1e-20	80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	rrm	RNA recognition motif.	1.2e-31	118.5
135	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
136	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	287.5
141	Peptidase_S26	Signal peptidase I	5.7e-10	35.7
143	arf	ADP-ribosylation factor family	1.2e-39	145.2
146	KRAB	KRAB box	7.3e-30	112.6
148	DUF6	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
151	S4	S4 domain	1.1e-08	42.3
153	tRNA-synt_1d	tRNA synthetases class I (R)	3.8e-103	356.1
154	Cyt_reductase	FAD/NAD-binding Cytochrome reductase	7.8e-60	212.2
155	ras	Ras family	3.6e-28	107.0
157	actin	Actin	3.8e-26	87.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn_carbOpept	Zinc carboxypeptidase	5e-138	471.9
165	pkinase	Eukaryotic protein kinase domain	5.1e-67	236.1
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S15	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	1e-48	157.0
171	DUF59	Domain of unknown function DUF59	0.07	-17.4
172	pkinase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	1e-31	118.8
178	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	C1q	C1q domain	8.8e-72	251.9
190	Y_phosphatase	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine dimethylases	0.00018	18.9
200	acid_phosphat	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP-synt_AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP-synt_AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	C1q	C1q domain	1.6e-70	247.7
212	UQ_con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ_con	Ubiquitin-conjugating enzyme	1e-53	191.9
215	DEAD	DEAD/DEAH box helicase	1.8e-43	140.4
216	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_transf_2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0.092	10.7
222	WD40	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGXG	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGXG	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHPx	Glutathione peroxidases	3.4e-47	170.2
231	tsp_1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
235	LRR	Leucine Rich Repeat	1.2e-30	115.3
236	LRR	Leucine Rich Repeat	6.7e-29	109.4
237	PDZ	PDZ domain (Also known as DHR or GLGF).	1.7e-09	45.0

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_deam	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekinase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflux	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid transporter protein	2.6e-52	187.2
258	adenylatekinase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQQ	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kinase	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase domain	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_transf_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymeraseX	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.1e-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRomatin Organization MOdifier)	4e-18	66.7
333	Peptidase_M12	Glycoprotease family	1.2e-136	467.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
335	vwa	von Willebrand factor type A domain	2.3e-07	37.9
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUF6	0.033	15.8
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	79.4
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	EF hand	5.4e-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin_G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0
376	ion_trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin-transferase).	1.3e-07	-13.5
384	ank	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-06	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	1.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.1e-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
399	fn3	Fibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	E1_dehydrog	Dehydrogenase E1 component	3e-119	409.6
402	fn3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
411	F-box	F-box domain.	4.2e-06	33.7
412	SNF2_N	SNF2 and others N-terminal domain	5.8e-16	61.6
415	CPSase_L_chain	Carbamoyl-phosphate synthase (CPSase)	1.5e-172	586.6
418	LRR	Leucine Rich Repeat	3.8e-24	93.6
419	DENN	DENN (AEX-3) domain	2e-58	207.5
420	RasGEF	RasGEF domain	8.1e-43	155.7
421	ank	Ank repeat	1.4e-153	523.7
424	G-patch	G-patch domain	1e-19	78.9
425	pkinase	Eukaryotic protein kinase domain	2.2e-31	117.1
426	Plexin_repeat	Plexin repeat	0.0023	24.6
427	Plexin_repea	Plexin repeat	0.0023	24.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	t			
429	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.6e-11	39.2
431	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
433	GTP_CDC	Cell division protein	2.1e-114	383.5
436	Collagen	Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin_B_lect in	Similarity to lectin domain of ricin b	0.0085	10.5
441	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	1.2e-256	866.0
442	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON) domain	0.00012	-17.1
446	ig	Immunoglobulin domain	0.00011	20.1
451	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_de c	Pyridoxal-dependent decarboxylase conse	8.3e-14	50.3
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion-channel	1e-175	597.1
458	Josephin	Josephin	0.0002	18.7
468	bZIP	bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer ase	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	1e-31	118.8
481	ArfGap	Putative GTP-ase activating protein for Arf	8.4e-66	232.0
485	SH2	Src homology domain 2	0.011	11.4
486	C1q	C1q domain	4.3e-74	259.6
487	dsrm	Double-stranded RNA binding motif	1.1e-47	171.9
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	ENV_polyprot ein	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_ 2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	39.5
504	abhydrolase	alpha/beta hydrolase fold	0.045	-3.6
505	vwa	von Willebrand factor type A domain	7.1e-62	219.0
508	Na_K_ATPase_ C	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201.5
510	Glycos_trans f_1	Glycosyl transferases group 1	2.9e-06	27.0
511	Glycos_trans f_1	Glycosyl transferases group 1	2.9e-06	27.0
512	Glycos_trans f_1	Glycosyl transferases group 1	1.9e-09	38.5
514	pro_isomeras e	Cyclophilin type peptidyl-prolyl cis-tr	1.8e-63	221.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	ig	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.1e-34	128.6
528	adh_zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha motif)	0.046	10.0
531	adh_short	short chain dehydrogenase	0.0025	-34.1
532	mito_carr	Mitochondrial carrier proteins	2.5e-81	281.7
533	mito_carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	PMO-like	Flavin-binding monooxygenase-like	0	1193.7
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
538	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
539	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	1.9e-117	403.6
540	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function DUF101	8.5e-38	139.0
545	TGFb_propept ide	TGF-beta propeptide	1.1e-67	238.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120.8
548	RHD	Rel homology domain (RHD).	1.6e-238	686.2
549	MMR_HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-transferase).	4.3e-127	435.6
554	MHC_II_alpha	Class II histocompatibility antigen, alp	3.5e-74	259.8
555	zf-UBR1	Putative zinc finger in N-recognin	3.3e-16	67.3
556	Kelch	Kelch motif	5.5e-29	109.7
561	AMP-binding	AMP-binding enzyme	2.8e-06	-163.7
562	PABP	Poly-adenylate binding protein, unique domai	4.9e-38	139.8
564	Gag_p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain	8.1e-16	66.0
567	SCAN	SCAN domain	7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
570	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	91.5
577	DNA_pol_B	DNA polymerase family B	0	1138.6
578	PDZ	PDZ domain (Also known as DHR or GLGF).	8.3e-09	42.7
579	LRR	Leucine Rich Repeat	4.9e-21	83.3
580	neur_chan	Neurotransmitter-gated ion-channel	5.9e-177	601.3
583	sushi	Sushi domain (SCR repeat)	0	1673.0
584	DEAD	DEAD/DEAH box helicase	7.3e-36	116.3
586	KH-domain	KH domain	2.9e-13	57.5
587	G-patch	G-patch domain	2.3e-14	61.2
589	LIM	LIM domain containing proteins	2.3e-36	133.4
590	bromodomain	Bromodomain	6.6e-32	114.7
591	bromodomain	Bromodomain	6.6e-32	114.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
592	hormone_rec	Ligand-binding domain of nuclear hormone	3.5e-22	87.1
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_binding	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatase	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623	BNR	BNR repeat	2.1e-11	51.3
624	molybdopterin	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork_head	Fork head domain	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal domain	1.2e-101	351.1
648	PseudoU_synth_2	RNA pseudouridylate synthase	1.9e-55	197.6
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion-channel	4.1e-171	581.8
654	tsp_1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670	spectrin	Spectrin repeat	4e-57	203.2
671	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC_tran	ABC transporter	5.3e-60	212.8
674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
676	LRR	Leucine Rich Repeat	0.0015	25.2
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-29	107.7
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPc	Dual specificity phosphatase, catalytic doma	4.3e-43	156.6
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PR55	Protein phosphatase 2A regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase_M24	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl_transf	Acyl transferase domain	1.1e-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran_BP1	RanBP1 domain.	8.4e-06	-7.3
713	DEAD	DEAD/DEAH box helicase	9.9e-42	134.9
714	PH	PH domain	1.6e-09	39.0
715	DSPc	Dual specificity phosphatase, catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	ig	Immunoglobulin domain	1e-29	100.8
719	integrin_B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Nop	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop	Putative snoRNA binding domain	8.1e-58	205.5
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	dsrm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
735	CDP-OH_P_transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
738	DEAD	DEAD/DEAH box helicase	8.6e-57	192.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI_typeI	Phosphomannose isomerase type I	1.2e-243	822.9
747	trypsin	Trypsin	6.4e-88	279.4
748	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
751	PHD	PHD-finger	4.9e-16	66.7
752	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	83.9
753	Hydrolase	haloacid dehalogenase-like hydrolase	6.1e-11	49.8
754	Ribosomal_L39	Ribosomal L39 protein	0.00018	26.7
755	PH	PH domain	3.6e-14	55.7
758	SCAN	SCAN domain	1.4e-53	191.5
759	PA	PA domain	0.0065	23.1
760	arf	ADP-ribosylation factor family	2.2e-19	77.8
761	CIDE-N	CIDE-N domain	2.2e-40	147.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	pou	Pou domain - N-terminal to homeobox domain	1e-52	188.6
767	vwc	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	1e-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD	Glucose-6-phosphate dehydrogenase	1.5e-76	256.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase_HII	Ribonuclease HII	2.5e-67	237.1
790	PI3_PI4_kinase	Phosphatidylinositol 3- and 4-kinases	5.4e-108	372.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-bind_lectin	Vertebrate galactoside-binding lectin	4.1e-25	88.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN_hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HMF	Histone-like transcription factor	6e-14	59.8
812	adh_short	short chain dehydrogenase	8.1e-20	79.3
814	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hydro	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF2	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-57	204.2
839	rrm	RNA recognition motif.	1.3e-22	88.5
840	Y_phosphatase	Protein-tyrosine phosphatase	2.6e-119	409.8
841	pkinase	Eukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L22e	Ribosomal L22e protein family	1e-64	228.4
846	IBR	IBR domain	9e-15	62.5
849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	18.9
851	SET	SET domain	5e-30	113.2
852	SRCR	Scavenger receptor cysteine-rich domain	0	1025.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		rich domain		
853	SRCR	Scavenger receptor cysteine-rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit VIa	3.4e-58	206.7
859	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito_carr	Mitochondrial carrier proteins	2.9e-51	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_chain	Carbamoyl-phosphate synthase (CPSase)	2.1e-218	739.0
879	Ribosomal_S12e	Ribosomal protein S12e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
884	RA	Ras association (RalGDS/AF-6) domain	0.044	8.0
887	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function DUF28	1.3e-43	156.3
896	IP_trans	Phosphatidylinositol transfer protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
899	KE2	KE2 family protein	7e-61	215.7
900	KE2	KE2 family protein	4.3e-51	183.2
901	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902	ras	Ras family	2.3e-75	263.8
904	TPR	TPR Domain	3.2e-22	87.2
906	GBP	Guanylate-binding protein	8.9e-253	853.1
907	GBP	Guanylate-binding protein	1.1e-239	809.6
908	WD40	WD domain, G-beta repeat	2.6e-26	100.8
909	PH	PH domain	1.3e-09	39.4
910	zf-C2H2	Zinc finger, C2H2 type	2.5e-39	144.1
913	Epimerase	NAD dependent epimerase/dehydratase family	5e-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
923	WD40	WD domain, G-beta repeat	8.2e-07	36.1
924	Hydrolase	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e-53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_epim	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul_P_3_epim	Ribulose-phosphate 3 epimerase family	1.2e-96	334.4
936	C2	C2 domain	2.2e-62	220.7
937	NAP_family	Nucleosome assembly protein (NAP)	1.1e-22	84.6
940	abhydrolase	alpha/beta hydrolase fold	0.011	3.1
944	Tropomyosin	Tropomyosins	3.2e-07	25.1
948	pkinase	Eukaryotic protein kinase domain	3.4e-75	263.2
949	WD40	WD domain, G-beta repeat	1.8e-27	104.7
950	Acyltransferase	Acyltransferase	1.6e-07	38.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO_IDH_MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-OH_P_transf	CDP-alcohol phosphatidyltransferase	0.053	-22.2
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh_short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969	IF-2B	Initiation factor 2 subunit family	8.4e-193	653.9
970	RNase_PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L17	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestrin	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_endo	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6) domain	1.2e-15	65.4
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.7e-15	53.1
1016	tRNA-synt_2c	tRNA synthetases class II (A)	2.3e-15	55.2
1018	RhoGAP	RhoGAP domain	1.6e-78	274.3
1022	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1026	HMG_box	HMG (high mobility group) box	8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028	UQ_con	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1032	PDZ	PDZ domain (Also known as DHR or GLGF).	0.028	16.3
1034	Hydrolase	haloacid dehalogenase-like hydrolase	2e-21	84.6
1037	KRAB	KRAB box	4.8e-06	32.4
1038	Cation_efflux	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADP-ribosyltransferase	4.7e-47	169.1
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1043	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin_c	Lectin C-type domain	1.9e-28	108.0
1046	Glucosamine_iso	Glucosamine-6-phosphate isomerase	0.00013	-25.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal_L24e	Ribosomal protein L24e	2e-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransferase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1_OBG	GTP1/OBG family	4.8e-41	141.8
1071	ig	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.8e-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPc	Dual specificity phosphatase, catalytic doma	3.3e-63	223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreductase	Nitroreductase family	1.3e-13	58.6
1106	PTB	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKc	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolase	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_sub	Adaptor complexes medium subunit family	1.2e-256	866.0
1137	Adap_comp_sub	Adaptor complexes medium subunit family	2.5e-209	708.8
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransferase	Acyltransferase	1.2e-05	29.9
1153	IRS	PTB domain (IRS-1 type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase_2	Asparaginase	6.4e-72	252.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3
1160	zf-AN1	AN1-like Zinc finger	0.00021	27.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1163	linker_histone	linker histone H1 and H5 family	3.8e-14	60.4
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf_8	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh_short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie_methyltran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP-synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN	SCAN domain	1.5e-71	251.1
1223	G-gamma	GGL domain	3.6e-36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
1236	PCH	Pas/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M20	Peptidase family M20/M25/M40	2e-63	224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown function UPF0006	6.3e-61	215.8
1248	Glycos_transf_2	Glycosyl transferases	4.5e-10	46.9
1249	efhand	EF hand	4e-11	50.4
1254	UQ_con	Ubiquitin-conjugating enzyme	2.1e-73	257.3
1255	ras	Ras family	2.2e-62	220.7
1256	formyl_transf	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
1261	DIHfolate_red	Dihydrofolate reductase	2.1e-69	241.7
1262	G_glu_transpept	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1263	PAS	PAS domain	1.3e-08	36.9
1265	LRR	Leucine Rich Repeat	4.2e-22	86.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
1267	K_tetra	K+ channel tetramerisation domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine-binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.1e-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L13	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_seg	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_synthetase	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_synthetase	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPc	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band_41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUF6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated macrophage pro	1.2e-202	686.6
1353	S_100	S-100/ICaBP type calcium binding domain	5.3e-23	89.9
1355	DEAD	DEAD/DEAH box helicase	3.6e-65	209.0
1356	C2	C2 domain	2.4e-15	64.4
1357	RBD	Raf-like Ras-binding domain	4.2e-57	203.1
1360	zf-C2H2	Zinc finger, C2H2 type	7.4e-141	481.4
1361	HMG14_17	HMG14 and HMG17	7.9e-40	145.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1362	SIS	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	ig	Immunoglobulin domain	0.00026	19.0
1368	K_tetra	K+ channel tetramerisation domain	1.1e-16	68.9
1371	Collagen	Collagen triple helix repeat (20 copies)	2.2e-113	390.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-09	35.6
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kinesin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1398	KRAB	KRAB box	5.1e-22	86.6
1402	bZIP	bZIP transcription factor	0.035	13.1
1405	sugar_tr	Sugar (and other) transporter	0.003	-101.5
1406	RhoGAP	RhoGAP domain	8.9e-47	168.8
1407	rrm	RNA recognition motif.	1e-35	132.1
1408	LRR	Leucine Rich Repeat	2.1e-13	58.0
1409	Nebulin_repeat	Nebulin repeat	6e-54	192.6
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal_L5_C	ribosomal L5P family C-terminus	8.2e-58	205.5
1415	trypsin	Trypsin	4.7e-85	270.4
1416	aminotran_1	Aminotransferases class-I	4.4e-05	-91.2
1417	S1	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating protein for Arf	1e-37	138.8
1428	helicase_C	Helicases conserved C-terminal domain	1e-26	102.2
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol_P	Inositol monophosphatase family	2.5e-10	40.2
1431	mito_carr	Mitochondrial carrier proteins	4.3e-83	287.7
1433	C1q	C1q domain	2.9e-16	66.2
1434	WD40	WD domain, G-beta repeat	1.6e-13	58.3
1435	Inos-1-P_synth	Myo-inositol-1-phosphate synthase	7e-228	770.4
1436	rrm	RNA recognition motif.	1.4e-34	128.3
1438	ig	Immunoglobulin domain	1.3e-12	45.6
1440	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1441	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1443	Kelch	Kelch motif	0.00013	28.7
1446	ARID	ARID DNA binding domain	1.8e-21	84.7
1447	zf-C2H2	Zinc finger, C2H2 type	9.4e-28	105.6
1448	AMP-binding	AMP-binding enzyme	2.6e-07	-145.1
1451	rrm	RNA recognition motif.	6.5e-21	82.9
1454	ig	Immunoglobulin domain	5.6e-44	146.7
1455	Sialyltransf	Sialyltransferase family	5.4e-21	83.2
1460	Aldose_epim	Aldose 1-epimerase	1.9e-35	131.2
1461	C2	C2 domain	4e-18	73.6
1470	TIG	IPT/TIG domain	3.1e-19	77.3
1472	PseudoU_synt	RNA pseudouridylate synthase	4.3e-16	66.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	h_2			
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation_efflux	Cation efflux family	4.6e-49	176.4
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_alpha	Telomere-binding protein alpha subuni	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase domain	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cyc	Adenylate and Guanylate cyclase catalyt	5.9e-46	166.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1e-10	36.5
1497	pkinase	Eukaryotic protein kinase domain	1e-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	2.7e-23	90.8
1506	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.7e-21	84.2
1508	Peptidase_M20	Peptidase family M20/M25/M40	2.8e-28	101.8
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35	130.7
1516	Syntaxin	Syntaxin	0.011	-62.3
1518	aminotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	365.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6) domain	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	10.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKc	Diacylglycerol kinase catalytic domain	6e-07	36.5
1540	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1653	SAP	SAP domain	6e-06	33.2
1654	Amino_oxidase	Flavin containing amine oxidase	3.2e-43	157.0
1655	Amino_oxidase	Flavin containing amine oxidase	3.2e-43	157.0
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR_HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.5e-11	51.1
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A domain	0	1909.4
1663	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1667	zf-C2H2	Zinc finger, C2H2 type	1.3e-93	324.4
1669	Nol1_Nop2_Sun	NOL1/NOP2/sun family	1.3e-23	84.3
1671	SH2	Src homology domain 2	5.4e-15	46.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1672	chromo	'chromo' (CHRromatin Organization MOdifier)	2.1e-18	67.7
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.0025	17.6
1676	Glyco_hydro_47	Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_47	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR_HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduct	Ferric reductase like transmembrane com	8.4e-82	285.2
1698	Ferric_reduct	Ferric reductase like transmembrane com	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	dsrm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacetyl	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	16.1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	176.9
1746	adh_short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1761	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1765	MMR_HSR1	GTPase of unknown function	6.4e-41	149.4
1769	CN_hydrolase	Carbon-nitrogen hydrolase	3e-06	-43.9
1775	ank	Ank repeat	4.1e-07	37.1
1779	Oxysterol_BP	Oxysterol-binding protein	4.7e-56	199.6
1783	RhoGEF	RhoGEF domain	1.6e-23	91.6
1784	RhoGEF	RhoGEF domain	1.6e-23	91.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN011.DOC)

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
11	1-23	0.989	0.899
12	1-25	0.955	0.803
13	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.970	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.984	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
187	1-28	0.982	0.936
190	1-19	0.953	0.840
196	1-22	0.975	0.916
197	1-22	0.963	0.936

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.803	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304	1-16	0.907	0.615
312	1-19	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.924
349	1-24	0.982	0.966
351	1-21	0.918	0.815
352	1-31	0.988	0.912
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.861	0.715
364	1-33	0.978	0.841
365	1-33	0.978	0.841

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	0.933
428	1-38	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498	1-26	0.993	0.890
505	1-20	0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0.556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.995	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677	1-16	0.948	0.807
685	1-21	0.881	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.880	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
719	1-20	0.961	0.824
729	1-29	0.972	0.874
735	1-46	0.903	0.598
746	1-14	0.916	0.730
747	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
864	1-20	0.928	0.782
866	1-19	0.986	0.934
873	1-23	0.948	0.686
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
981	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
1052	1-18	0.969	0.842
1059	1-20	0.929	0.867
1065	1-33	0.983	0.918
1069	1-22	0.993	0.935

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	0.899
1430	1-34	0.977	0.818
1431	1-28	0.979	0.923
1432	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.983	0.621
1435	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
1580	1-17	0.923	0.824
1593	1-28	0.979	0.923

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.919	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TABLE 6

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1	1787	3573	5359	784CIP2_1	1103
2	1788	3574	5360	784CIP2_2	2673
3	1789	3575	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2_5	5562
6	1792	3578	5364	784CIP2_6	5562
7	1793	3579	5365	784CIP2_7	5562
8	1794	3580	5366	784CIP2_8	5562
9	1795	3581	5367	784CIP2_9	5563
10	1796	3582	5368	784CIP2_10	5564
11	1797	3583	5369	784CIP2_11	5565
12	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1800	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2_20	5805
21	1807	3593	5379	784CIP2_21	5805
22	1808	3594	5380	784CIP2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382	784CIP2_24	5850
25	1811	3597	5383	784CIP2_25	5867
26	1812	3598	5384	784CIP2_26	5973
27	1813	3599	5385	784CIP2_27	5995
28	1814	3600	5386	784CIP2_28	5995
29	1815	3601	5387	784CIP2_29	6005
30	1816	3602	5388	784CIP2_30	6007
31	1817	3603	5389	784CIP2_31	6007
32	1818	3604	5390	784CIP2_32	6009
33	1819	3605	5391	784CIP2_33	6012
34	1820	3606	5392	784CIP2_34	6015
35	1821	3607	5393	784CIP2_35	6016
36	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	784CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2_49	6191
50	1836	3622	5408	784CIP2_50	6204
51	1837	3623	5409	784CIP2_51	6204
52	1838	3624	5410	784CIP2_52	6284
53	1839	3625	5411	784CIP2_53	6367
54	1840	3626	5412	784CIP2_54	6436
55	1841	3627	5413	784CIP2_55	6442
56	1842	3628	5414	784CIP2_56	6445
57	1843	3629	5415	784CIP2_57	6457
58	1844	3630	5416	784CIP2_58	6458
59	1845	3631	5417	784CIP2_59	6458

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
60	1846	3632	5418	784CIP2_60	6462
61	1847	3633	5419	784CIP2_61	6472
62	1848	3634	5420	784CIP2_62	6499
63	1849	3635	5421	784CIP2_63	6499
64	1850	3636	5422	784CIP2_64	6505
65	1851	3637	5423	784CIP2_65	6534
66	1852	3638	5424	784CIP2_66	6534
67	1853	3639	5425	784CIP2_67	6540
68	1854	3640	5426	784CIP2_68	6550
69	1855	3641	5427	784CIP2_69	6550
70	1856	3642	5428	784CIP2_70	6592
71	1857	3643	5429	784CIP2_71	6645
72	1858	3644	5430	784CIP2_72	6671
73	1859	3645	5431	784CIP2_73	6763
74	1860	3646	5432	784CIP2_74	6763
75	1861	3647	5433	784CIP2_75	6786
76	1862	3648	5434	784CIP2_76	6824
77	1863	3649	5435	784CIP2_77	6830
78	1864	3650	5436	784CIP2_78	6831
79	1865	3651	5437	784CIP2_79	6832
80	1866	3652	5438	784CIP2_80	6834
81	1867	3653	5439	784CIP2_81	6834
82	1868	3654	5440	784CIP2_82	6835
83	1869	3655	5441	784CIP2_83	6837
84	1870	3656	5442	784CIP2_84	6843
85	1871	3657	5443	784CIP2_85	6859
86	1872	3658	5444	784CIP2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784CIP2_88	6957
89	1875	3661	5447	784CIP2_89	6961
90	1876	3662	5448	784CIP2_90	6973
91	1877	3663	5449	784CIP2_91	6973
92	1878	3664	5450	784CIP2_93	7007
93	1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2_95	7019
95	1881	3667	5453	784CIP2_96	7020
96	1882	3668	5454	784CIP2_97	7020
97	1883	3669	5455	784CIP2_98	7021
98	1884	3670	5456	784CIP2_99	7023
99	1885	3671	5457	784CIP2_100	7027
100	1886	3672	5458	784CIP2_101	7028
101	1887	3673	5459	784CIP2_102	7029
102	1888	3674	5460	784CIP2_103	7031
103	1889	3675	5461	784CIP2_104	7032
104	1890	3676	5462	784CIP2_105	7033
105	1891	3677	5463	784CIP2_106	7035
106	1892	3678	5464	784CIP2_107	7036
107	1893	3679	5465	784CIP2_108	7039
108	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	7044
110	1896	3682	5468	784CIP2_111	7046
111	1897	3683	5469	784CIP2_112	7054
112	1898	3684	5470	784CIP2_113	7061
113	1899	3685	5471	784CIP2_114	7077
114	1900	3686	5472	784CIP2_115	7092
115	1901	3687	5473	784CIP2_116	7094
116	1902	3688	5474	784CIP2_117	7106
117	1903	3689	5475	784CIP2_118	7107
118	1904	3690	5476	784CIP2_119	7111
119	1905	3691	5477	784CIP2_120	7123
120	1906	3692	5478	784CIP2_121	7142
121	1907	3693	5479	784CIP2_122	7142

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
122	1908	3694	5480	784CIP2_123	7154
123	1909	3695	5481	784CIP2_124	7160
124	1910	3696	5482	784CIP2_125	7169
125	1911	3697	5483	784CIP2_126	7185
126	1912	3698	5484	784CIP2_127	7197
127	1913	3699	5485	784CIP2_128	7219
128	1914	3700	5486	784CIP2_129	7226
129	1915	3701	5487	784CIP2_130	7229
130	1916	3702	5488	784CIP2_131	7234
131	1917	3703	5489	784CIP2_132	7235
132	1918	3704	5490	784CIP2_133	7235
133	1919	3705	5491	784CIP2_134	7238
134	1920	3706	5492	784CIP2_135	7247
135	1921	3707	5493	784CIP2_136	7261
136	1922	3708	5494	784CIP2_137	7262
137	1923	3709	5495	784CIP2_138	7267
138	1924	3710	5496	784CIP2_139	7272
139	1925	3711	5497	784CIP2_140	7273
140	1926	3712	5498	784CIP2_141	7282
141	1927	3713	5499	784CIP2_142	7288
142	1928	3714	5500	784CIP2_143	7291
143	1929	3715	5501	784CIP2_144	7293
144	1930	3716	5502	784CIP2_145	7294
145	1931	3717	5503	784CIP2_146	7299
146	1932	3718	5504	784CIP2_147	7300
147	1933	3719	5505	784CIP2_148	7312
148	1934	3720	5506	784CIP2_149	7313
149	1935	3721	5507	784CIP2_150	7315
150	1936	3722	5508	784CIP2_151	7318
151	1937	3723	5509	784CIP2_152	7321
152	1938	3724	5510	784CIP2_153	7330
153	1939	3725	5511	784CIP2_154	7331
154	1940	3726	5512	784CIP2_155	7333
155	1941	3727	5513	784CIP2_156	7350
156	1942	3728	5514	784CIP2_157	7352
157	1943	3729	5515	784CIP2_158	7384
158	1944	3730	5516	784CIP2_159	7403
159	1945	3731	5517	784CIP2_160	7431
160	1946	3732	5518	784CIP2_161	7441
161	1947	3733	5519	784CIP2_162	7453
162	1948	3734	5520	784CIP2_163	7467
163	1949	3735	5521	784CIP2_164	7471
164	1950	3736	5522	784CIP2_165	7493
165	1951	3737	5523	784CIP2_166	7502
166	1952	3738	5524	784CIP2_167	7511
167	1953	3739	5525	784CIP2_168	7514
168	1954	3740	5526	784CIP2_169	7520
169	1955	3741	5527	784CIP2_170	7541
170	1956	3742	5528	784CIP2_171	7570
171	1957	3743	5529	784CIP2_172	7578
172	1958	3744	5530	784CIP2_173	7583
173	1959	3745	5531	784CIP2_174	7592
174	1960	3746	5532	784CIP2_175	7601
175	1961	3747	5533	784CIP2_176	7602
176	1962	3748	5534	784CIP2_177	7608
177	1963	3749	5535	784CIP2_178	7615
178	1964	3750	5536	784CIP2_179	7617
179	1965	3751	5537	784CIP2_181	7624
180	1966	3752	5538	784CIP2_182	7626
181	1967	3753	5539	784CIP2_183	7640
182	1968	3754	5540	784CIP2_184	7641
183	1969	3755	5541	784CIP2_185	7641

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
184	1970	3756	5542	784CIP2_186	7641
185	1971	3757	5543	784CIP2_187	7642
186	1972	3758	5544	784CIP2_188	7649
187	1973	3759	5545	784CIP2_189	7656
188	1974	3760	5546	784CIP2_190	7657
189	1975	3761	5547	784CIP2_191	7659
190	1976	3762	5548	784CIP2_192	7662
191	1977	3763	5549	784CIP2_193	7668
192	1978	3764	5550	784CIP2_194	7673
193	1979	3765	5551	784CIP2_195	7690
194	1980	3766	5552	784CIP2_196	7700
195	1981	3767	5553	784CIP2_197	7709
196	1982	3768	5554	784CIP2_198	7736
197	1983	3769	5555	784CIP2_199	7737
198	1984	3770	5556	784CIP2_200	7744
199	1985	3771	5557	784CIP2_201	7771
200	1986	3772	5558	784CIP2_202	7786
201	1987	3773	5559	784CIP2_203	7791
202	1988	3774	5560	784CIP2_204	7797
203	1989	3775	5561	784CIP2_205	7806
204	1990	3776	5562	784CIP2_206	7812
205	1991	3777	5563	784CIP2_207	7812
206	1992	3778	5564	784CIP2_208	7818
207	1993	3779	5565	784CIP2_209	7822
208	1994	3780	5566	784CIP2_210	7827
209	1995	3781	5567	784CIP2_211	7830
210	1996	3782	5568	784CIP2_212	7835
211	1997	3783	5569	784CIP2_214	7840
212	1998	3784	5570	784CIP2_215	7858
213	1999	3785	5571	784CIP2_216	7858
214	2000	3786	5572	784CIP2_217	7861
215	2001	3787	5573	784CIP2_218	7866
216	2002	3788	5574	784CIP2_219	7868
217	2003	3789	5575	784CIP2_220	7896
218	2004	3790	5576	784CIP2_221	7898
219	2005	3791	5577	784CIP2_222	7900
220	2006	3792	5578	784CIP2_223	7906
221	2007	3793	5579	784CIP2_224	7908
222	2008	3794	5580	784CIP2_225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2_243	8137
241	2027	3813	5599	784CIP2_244	8137
242	2028	3814	5600	784CIP2_245	8159
243	2029	3815	5601	784CIP2_246	8159
244	2030	3816	5602	784CIP2_247	8161
245	2031	3817	5603	784CIP2_248	8176

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
246	2032	3818	5604	784CIP2_249	8196
247	2033	3819	5605	784CIP2_250	8200
248	2034	3820	5606	784CIP2_251	8212
249	2035	3821	5607	784CIP2_252	8220
250	2036	3822	5608	784CIP2_253	8238
251	2037	3823	5609	784CIP2_254	8254
252	2038	3824	5610	784CIP2_255	8255
253	2039	3825	5611	784CIP2_256	8288
254	2040	3826	5612	784CIP2_257	8296
255	2041	3827	5613	784CIP2_258	8329
256	2042	3828	5614	784CIP2_259	8362
257	2043	3829	5615	784CIP2_260	8429
258	2044	3830	5616	784CIP2_261	8436
259	2045	3831	5617	784CIP2_262	8448
260	2046	3832	5618	784CIP2_263	8472
261	2047	3833	5619	784CIP2_264	8502
262	2048	3834	5620	784CIP2_265	8504
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269	2055	3841	5627	784CIP2_273	8532
270	2056	3842	5628	784CIP2_274	8539
271	2057	3843	5629	784CIP2_275	8541
272	2058	3844	5630	784CIP2_276	8543
273	2059	3845	5631	784CIP2_277	8593
274	2060	3846	5632	784CIP2_278	8595
275	2061	3847	5633	784CIP2_279	8615
276	2062	3848	5634	784CIP2_280	8620
277	2063	3849	5635	784CIP2_281	8621
278	2064	3850	5636	784CIP2_282	8623
279	2065	3851	5637	784CIP2_283	8625
280	2066	3852	5638	784CIP2_284	8628
281	2067	3853	5639	784CIP2_285	8628
282	2068	3854	5640	784CIP2_286	8629
283	2069	3855	5641	784CIP2_287	8630
284	2070	3856	5642	784CIP2_288	8631
285	2071	3857	5643	784CIP2_289	8633
286	2072	3858	5644	784CIP2_290	8634
287	2073	3859	5645	784CIP2_291	8635
288	2074	3860	5646	784CIP2_292	8636
289	2075	3861	5647	784CIP2_293	8659
290	2076	3862	5648	784CIP2_294	8660
291	2077	3863	5649	784CIP2_295	8667
292	2078	3864	5650	784CIP2_296	8667
293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2_298	8805
295	2081	3867	5653	784CIP2_299	8896
296	2082	3868	5654	784CIP2_300	8978
297	2083	3869	5655	784CIP2_301	9046
298	2084	3870	5656	784CIP2_302	9048
299	2085	3871	5657	784CIP2_303	9116
300	2086	3872	5658	784CIP2_304	9195
301	2087	3873	5659	784CIP2_305	9201
302	2088	3874	5660	784CIP2_306	9307
303	2089	3875	5661	784CIP2_307	9321
304	2090	3876	5662	784CIP2_308	9397
305	2091	3877	5663	784CIP2_309	9405
306	2092	3878	5664	784CIP2_310	9406
307	2093	3879	5665	784CIP2_311	9422

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
308	2094	3880	5666	784CIP2_312	9494
309	2095	3881	5667	784CIP2_313	9512
310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5676	784CIP2_322	9887
319	2105	3891	5677	784CIP2_323	9923
320	2106	3892	5678	784CIP2_324	9938
321	2107	3893	5679	784CIP2_325	9964
322	2108	3894	5680	784CIP2_326	10007
323	2109	3895	5681	784CIP2_327	10009
324	2110	3896	5682	784CIP2_328	10046
325	2111	3897	5683	784CIP2_329	10156
326	2112	3898	5684	784CIP2_330	10276
327	2113	3899	5685	784CIP2_331	10283
328	2114	3900	5686	784CIP2B_1	152
329	2115	3901	5687	784CIP2B_2	167
330	2116	3902	5688	7H4CIP2B_3	205
331	2117	3903	5689	784CIP2B_4	210
332	2118	3904	5690	784CIP2B_5	225
333	2119	3905	5691	784CIP2B_6	226
334	2120	3906	5692	784CIP2B_7	264
335	2121	3907	5693	784CIP2B_8	268
336	2122	3908	5694	784CIP2B_9	293
337	2123	3909	5695	784CIP2B_10	293
338	2124	3910	5696	784CIP2B_11	293
339	2125	3911	5697	784CIP2B_12	302
340	2126	3912	5698	784CIP2B_13	311
341	2127	3913	5699	784CIP2B_14	352
342	2128	3914	5700	784CIP2B_15	358
343	2129	3915	5701	784CIP2B_16	368
344	2130	3916	5702	784CIP2B_17	393
345	2131	3917	5703	784CIP2B_18	477
346	2132	3918	5704	784CIP2B_19	508
347	2133	3919	5705	784CIP2B_20	508
348	2134	3920	5706	784CIP2B_21	515
349	2135	3921	5707	784CIP2B_22	578
350	2136	3922	5708	784CIP2B_23	588
351	2137	3923	5709	784CIP2B_24	591
352	2138	3924	5710	784CIP2B_25	593
353	2139	3925	5711	784CIP2B_26	594
354	2140	3926	5712	784CIP2B_27	619
355	2141	3927	5713	784CIP2B_28	620
356	2142	3928	5714	784CIP2B_29	654
357	2143	3929	5715	784CIP2B_30	692
358	2144	3930	5716	784CIP2B_31	753
359	2145	3931	5717	784CIP2B_32	758
360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	813
362	2148	3934	5720	784CIP2B_35	838
363	2149	3935	5721	784CIP2B_36	870
364	2150	3936	5722	784CIP2B_37	891
365	2151	3937	5723	784CIP2B_38	891
366	2152	3938	5724	784CIP2B_39	921
367	2153	3939	5725	784CIP2B_40	924
368	2154	3940	5726	784CIP2B_41	932
369	2155	3941	5727	784CIP2B_42	942

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
370	2156	3942	5728	784CIP2B_43	958
371	2157	3943	5729	784CIP2B_44	968
372	2158	3944	5730	784CIP2B_45	992
373	2159	3945	5731	784CIP2B_46	1025
374	2160	3946	5732	784CIP2B_47	1074
375	2161	3947	5733	784CIP2B_48	1104
376	2162	3948	5734	784CIP2B_49	1114
377	2163	3949	5735	784CIP2B_50	1144
378	2164	3950	5736	784CIP2B_51	1262
379	2165	3951	5737	784CIP2B_52	1318
380	2166	3952	5738	784CIP2B_53	1319
381	2167	3953	5739	784CIP2B_54	1328
382	2168	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B_56	1464
384	2170	3956	5742	784CIP2B_57	1584
385	2171	3957	5743	784CIP2B_58	1617
386	2172	3958	5744	784CIP2B_59	1724
387	2173	3959	5745	784CIP2B_60	1728
388	2174	3960	5746	784CIP2B_61	1772
389	2175	3961	5747	784CIP2B_62	1809
390	2176	3962	5748	784CIP2B_63	1860
391	2177	3963	5749	784CIP2B_64	1898
392	2178	3964	5750	784CIP2B_65	1926
393	2179	3965	5751	784CIP2B_66	1965
394	2180	3966	5752	784CIP2B_67	1967
395	2181	3967	5753	784CIP2B_68	1995
396	2182	3968	5754	784CIP2B_69	2005
397	2183	3969	5755	784CIP2B_70	2027
398	2184	3970	5756	784CIP2B_71	2055
399	2185	3971	5757	784CIP2B_72	2103
400	2186	3972	5758	784CIP2B_73	2106
401	2187	3973	5759	784CIP2B_74	2166
402	2188	3974	5760	784CIP2B_75	2175
403	2189	3975	5761	784CIP2B_76	2176
404	2190	3976	5762	784CIP2B_78	2236
405	2191	3977	5763	784CIP2B_79	2250
406	2192	3978	5764	784CIP2B_80	2300
407	2193	3979	5765	784CIP2B_81	2323
408	2194	3980	5766	784CIP2B_82	2340
409	2195	3981	5767	784CIP2B_83	2371
410	2196	3982	5768	784CIP2B_84	2399
411	2197	3983	5769	784CIP2B_85	2411
412	2198	3984	5770	784CIP2B_86	2428
413	2199	3985	5771	784CIP2B_87	2430
414	2200	3986	5772	784CIP2B_88	2439
415	2201	3987	5773	784CIP2B_89	2447
416	2202	3988	5774	784CIP2B_90	2461
417	2203	3989	5775	784CIP2B_91	2487
418	2204	3990	5776	784CIP2B_92	2492
419	2205	3991	5777	784CIP2B_93	2512
420	2206	3992	5778	784CIP2B_94	2564
421	2207	3993	5779	784CIP2B_95	2678
422	2208	3994	5780	784CIP2B_96	2816
423	2209	3995	5781	784CIP2B_97	2818
424	2210	3996	5782	784CIP2B_98	2819
425	2211	3997	5783	784CIP2B_99	2943
426	2212	3998	5784	784CIP2B_100	3137
427	2213	3999	5785	784CIP2B_101	3137
428	2214	4000	5786	784CIP2B_102	3160
429	2215	4001	5787	784CIP2B_103	3323
430	2216	4002	5788	784CIP2B_104	3360
431	2217	4003	5789	784CIP2B_105	3362

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
432	2218	4004	5790	784CIP2B_106	3417
433	2219	4005	5791	784CIP2B_107	3418
434	2220	4006	5792	784CIP2B_108	3442
435	2221	4007	5793	784CIP2B_109	3442
436	2222	4008	5794	784CIP2B_110	3444
437	2223	4009	5795	784CIP2B_111	3855
438	2224	4010	5796	784CIP2B_112	3863
439	2225	4011	5797	784CIP2B_113	4090
440	2226	4012	5798	784CIP2B_114	4105
441	2227	4013	5799	784CIP2B_115	4142
442	2228	4014	5800	784CIP2B_116	4142
443	2229	4015	5801	784CIP2B_117	4149
444	2230	4016	5802	784CIP2B_118	4196
445	2231	4017	5803	784CIP2B_119	4202
446	2232	4018	5804	784CIP2B_120	4274
447	2233	4019	5805	784CIP2B_121	4304
448	2234	4020	5806	784CIP2B_122	4306
449	2235	4021	5807	784CIP2B_123	4311
450	2236	4022	5808	784CIP2B_124	4321
451	2237	4023	5809	784CIP2B_125	4323
452	2238	4024	5810	784CIP2B_126	4332
453	2239	4025	5811	784CIP2B_127	4488
454	2240	4026	5812	784CIP2B_128	4588
455	2241	4027	5813	784CIP2B_129	5569
456	2242	4028	5814	784CIP2B_130	5573
457	2243	4029	5815	784CIP2B_131	5577
458	2244	4030	5816	784CIP2B_132	5579
459	2245	4031	5817	784CIP2B_133	5582
460	2246	4032	5818	784CIP2B_134	5583
461	2247	4033	5819	784CIP2B_135	5584
462	2248	4034	5820	784CIP2B_136	5585
463	2249	4035	5821	784CIP2B_137	5591
464	2250	4036	5822	784CIP2B_138	5593
465	2251	4037	5823	784CIP2B_139	5594
466	2252	4038	5824	784CIP2B_140	5594
467	2253	4039	5825	784CIP2B_141	5598
468	2254	4040	5826	784CIP2B_142	5602
469	2255	4041	5827	784CIP2B_143	5605
470	2256	4042	5828	784CIP2B_144	5608
471	2257	4043	5829	784CIP2B_145	5617
472	2258	4044	5830	784CIP2B_146	5620
473	2259	4045	5831	784CIP2B_147	5622
474	2260	4046	5832	784CIP2B_148	5623
475	2261	4047	5833	784CIP2B_149	5624
476	2262	4048	5834	784CIP2B_150	5625
477	2263	4049	5835	784CIP2B_151	5627
478	2264	4050	5836	784CIP2B_152	5628
479	2265	4051	5837	784CIP2B_153	5630
480	2266	4052	5838	784CIP2B_154	5632
481	2267	4053	5839	784CIP2B_155	5640
482	2268	4054	5840	784CIP2B_156	5641
483	2269	4055	5841	784CIP2B_157	5643
484	2270	4056	5842	784CIP2B_158	5647
485	2271	4057	5843	784CIP2B_159	5649
486	2272	4058	5844	784CIP2B_160	5658
487	2273	4059	5845	784CIP2B_161	5659
488	2274	4060	5846	784CIP2B_162	5667
489	2275	4061	5847	784CIP2B_163	5672
490	2276	4062	5848	784CIP2B_164	5674
491	2277	4063	5849	784CIP2B_165	5678
492	2278	4064	5850	784CIP2B_166	5680
493	2279	4065	5851	784CIP2B_167	5684

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
494	2280	4066	5852	784CIP2B_168	5686
495	2281	4067	5853	784CIP2B_169	5694
496	2282	4068	5854	784CIP2B_170	5698
497	2283	4069	5855	784CIP2B_171	5699
498	2284	4070	5856	784CIP2B_172	5712
499	2285	4071	5857	784CIP2B_173	5719
500	2286	4072	5858	784CIP2B_174	5720
501	2287	4073	5859	784CIP2B_175	5727
502	2288	4074	5860	784CIP2B_176	5730
503	2289	4075	5861	784CIP2B_177	5734
504	2290	4076	5862	784CIP2B_178	5738
505	2291	4077	5863	784CIP2B_179	5739
506	2292	4078	5864	784CIP2B_180	5740
507	2293	4079	5865	784CIP2B_181	5744
508	2294	4080	5866	784CIP2B_182	5748
509	2295	4081	5867	784CIP2B_183	5749
510	2296	4082	5868	784CIP2B_184	5750
511	2297	4083	5869	784CIP2B_185	5750
512	2298	4084	5870	784CIP2B_186	5750
513	2299	4085	5871	784CIP2B_187	5761
514	2300	4086	5872	784CIP2B_188	5762
515	2301	4087	5873	784CIP2B_189	5767
516	2302	4088	5874	784CIP2B_190	5773
517	2303	4089	5875	784CIP2B_191	5783
518	2304	4090	5876	784CIP2B_192	5784
519	2305	4091	5877	784CIP2B_193	5788
520	2306	4092	5878	784CIP2B_194	5798
521	2307	4093	5879	784CIP2B_196	5807
522	2308	4094	5880	784CIP2B_197	5818
523	2309	4095	5881	784CIP2B_198	5819
524	2310	4096	5882	784CIP2B_199	5827
525	2311	4097	5883	784CIP2B_200	5828
526	2312	4098	5884	784CIP2B_201	5842
527	2313	4099	5885	784CIP2B_202	5853
528	2314	4100	5886	784CIP2B_203	5861
529	2315	4101	5887	784CIP2B_204	5864
530	2316	4102	5888	784CIP2B_205	5865
531	2317	4103	5889	784CIP2B_206	5871
532	2318	4104	5890	784CIP2B_207	5873
533	2319	4105	5891	784CIP2B_208	5873
534	2320	4106	5892	784CIP2B_209	5875
535	2321	4107	5893	784CIP2B_210	5878
536	2322	4108	5894	784CIP2B_211	5879
537	2323	4109	5895	784CIP2B_212	5880
538	2324	4110	5896	784CIP2B_213	5880
539	2325	4111	5897	784CIP2B_214	5880
540	2326	4112	5898	784CIP2B_215	5880
541	2327	4113	5899	784CIP2B_216	5885
542	2328	4114	5900	784CIP2B_217	5895
543	2329	4115	5901	784CIP2B_218	5898
544	2330	4116	5902	784CIP2B_219	5903
545	2331	4117	5903	784CIP2B_220	5904
546	2332	4118	5904	784CIP2B_221	5918
547	2333	4119	5905	784CIP2B_222	5921
548	2334	4120	5906	784CIP2B_223	5927
549	2335	4121	5907	784CIP2B_224	5932
550	2336	4122	5908	784CIP2B_225	5939
551	2337	4123	5909	784CIP2B_226	5945
552	2338	4124	5910	784CIP2B_227	5946
553	2339	4125	5911	784CIP2B_228	5947
554	2340	4126	5912	784CIP2B_229	5956
555	2341	4127	5913	784CIP2B_230	5967

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
556	2342	4128	5914	784CIP2B_232	5975
557	2343	4129	5915	784CIP2B_233	5977
558	2344	4130	5916	784CIP2B_234	5978
559	2345	4131	5917	784CIP2B_235	5979
560	2346	4132	5918	784CIP2B_236	5980
561	2347	4133	5919	784CIP2B_237	5988
562	2348	4134	5920	784CIP2B_238	5989
563	2349	4135	5921	784CIP2B_239	5991
564	2350	4136	5922	784CIP2B_240	5997
565	2351	4137	5923	784CIP2B_241	5998
566	2352	4138	5924	784CIP2B_242	6003
567	2353	4139	5925	784CIP2B_243	6004
568	2354	4140	5926	784CIP2B_244	6013
569	2355	4141	5927	784CIP2B_245	6028
570	2356	4142	5928	784CIP2B_246	6028
571	2357	4143	5929	784CIP2B_247	6029
572	2358	4144	5930	784CIP2B_248	6031
573	2359	4145	5931	784CIP2B_249	6031
574	2360	4146	5932	784CIP2B_250	6032
575	2361	4147	5933	784CIP2B_251	6037
576	2362	4148	5934	784CIP2B_252	6037
577	2363	4149	5935	784CIP2B_253	6043
578	2364	4150	5936	784CIP2B_254	6044
579	2365	4151	5937	784CIP2B_255	6046
580	2366	4152	5938	784CIP2B_256	6048
581	2367	4153	5939	784CIP2B_257	6049
582	2368	4154	5940	784CIP2B_258	6051
583	2369	4155	5941	784CIP2B_259	6053
584	2370	4156	5942	784CIP2B_260	6060
585	2371	4157	5943	784CIP2B_261	6063
586	2372	4158	5944	784CIP2B_262	6066
587	2373	4159	5945	784CIP2B_263	6067
588	2374	4160	5946	784CIP2B_264	6068
589	2375	4161	5947	784CIP2B_265	6073
590	2376	4162	5948	784CIP2B_266	6076
591	2377	4163	5949	784CIP2B_267	6076
592	2378	4164	5950	784CIP2B_268	6077
593	2379	4165	5951	784CIP2B_269	6079
594	2380	4166	5952	784CIP2B_270	6082
595	2381	4167	5953	784CIP2B_272	6088
596	2382	4168	5954	784CIP2B_273	6091
597	2383	4169	5955	784CIP2B_274	6094
598	2384	4170	5956	784CIP2B_275	6101
599	2385	4171	5957	784CIP2B_276	6103
600	2386	4172	5958	784CIP2B_277	6104
601	2387	4173	5959	784CIP2B_278	6108
602	2388	4174	5960	784CIP2B_279	6112
603	2389	4175	5961	784CIP2B_280	6121
604	2390	4176	5962	784CIP2B_281	6125
605	2391	4177	5963	784CIP2B_282	6126
606	2392	4178	5964	784CIP2B_283	6128
607	2393	4179	5965	784CIP2B_284	6129
608	2394	4180	5966	784CIP2B_285	6133
609	2395	4181	5967	784CIP2B_286	6133
610	2396	4182	5968	784CIP2B_287	6135
611	2397	4183	5969	784CIP2B_288	6139
612	2398	4184	5970	784CIP2B_289	6141
613	2399	4185	5971	784CIP2B_290	6145
614	2400	4186	5972	784CIP2B_291	6146
615	2401	4187	5973	784CIP2B_292	6148
616	2402	4188	5974	784CIP2B_293	6149
617	2403	4189	5975	784CIP2B_294	6149

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
618	2404	4190	5976	784CIP2B_295	6153
619	2405	4191	5977	784CIP2B_296	6159
620	2406	4192	5978	784CIP2B_297	6164
621	2407	4193	5979	784CIP2B_298	6167
622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B_300	6173
624	2410	4196	5982	784CIP2B_301	6190
625	2411	4197	5983	784CIP2B_302	6194
626	2412	4198	5984	784CIP2B_303	6196
627	2413	4199	5985	784CIP2B_304	6197
628	2414	4200	5986	784CIP2B_305	6198
629	2415	4201	5987	784CIP2B_306	6198
630	2416	4202	5988	784CIP2B_308	6214
631	2417	4203	5989	784CIP2B_309	6215
632	2418	4204	5990	784CIP2B_310	6219
633	2419	4205	5991	784CIP2B_311	6226
634	2420	4206	5992	784CIP2B_312	6229
635	2421	4207	5993	784CIP2B_313	6234
636	2422	4208	5994	784CIP2B_314	6237
637	2423	4209	5995	784CIP2B_315	6238
638	2424	4210	5996	784CIP2B_316	6239
639	2425	4211	5997	784CIP2B_317	6239
640	2426	4212	5998	784CIP2B_318	6239
641	2427	4213	5999	784CIP2B_319	6240
642	2428	4214	6000	784CIP2B_320	6244
643	2429	4215	6001	784CIP2B_321	6245
644	2430	4216	6002	784CIP2B_322	6250
645	2431	4217	6003	784CIP2B_323	6252
646	2432	4218	6004	784CIP2B_324	6252
647	2433	4219	6005	784CIP2B_325	6256
648	2434	4220	6006	784CIP2B_326	6260
649	2435	4221	6007	784CIP2B_327	6261
650	2436	4222	6008	784CIP2B_328	6264
651	2437	4223	6009	784CIP2B_329	6265
652	2438	4224	6010	784CIP2B_330	6266
653	2439	4225	6011	784CIP2B_331	6270
654	2440	4226	6012	784CIP2B_332	6271
655	2441	4227	6013	784CIP2B_334	6274
656	2442	4228	6014	784CIP2B_335	6276
657	2443	4229	6015	784CIP2B_336	6281
658	2444	4230	6016	784CIP2B_337	6281
659	2445	4231	6017	784CIP2B_338	6288
660	2446	4232	6018	784CIP2B_339	6292
661	2447	4233	6019	784CIP2B_340	6294
662	2448	4234	6020	784CIP2B_343	6312
663	2449	4235	6021	784CIP2B_344	6312
664	2450	4236	6022	784CIP2B_345	6312
665	2451	4237	6023	784CIP2B_346	6322
666	2452	4238	6024	784CIP2B_347	6324
667	2453	4239	6025	784CIP2B_349	6329
668	2454	4240	6026	784CIP2B_350	6331
669	2455	4241	6027	784CIP2B_351	6333
670	2456	4242	6028	784CIP2B_352	6334
671	2457	4243	6029	784CIP2B_353	6337
672	2458	4244	6030	784CIP2B_354	6339
673	2459	4245	6031	784CIP2B_355	6346
674	2460	4246	6032	784CIP2B_356	6348
675	2461	4247	6033	784CIP2B_357	6348
676	2462	4248	6034	784CIP2B_358	6350
677	2463	4249	6035	784CIP2B_359	6351
678	2464	4250	6036	784CIP2B_360	6355
679	2465	4251	6037	784CIP2B_361	6362

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
680	2466	4252	6038	784CIP2B_362	6368
681	2467	4253	6039	784CIP2B_363	6369
682	2468	4254	6040	784CIP2B_364	6371
683	2469	4255	6041	784CIP2B_365	6376
684	2470	4256	6042	784CIP2B_366	6379
685	2471	4257	6043	784CIP2B_367	6380
686	2472	4258	6044	784CIP2B_368	6381
687	2473	4259	6045	784CIP2B_369	6392
688	2474	4260	6046	784CIP2B_370	6395
689	2475	4261	6047	784CIP2B_371	6397
690	2476	4262	6048	784CIP2B_372	6400
691	2477	4263	6049	784CIP2B_373	6401
692	2478	4264	6050	784CIP2B_374	6411
693	2479	4265	6051	784CIP2B_375	6411
694	2480	4266	6052	784CIP2B_376	6411
695	2481	4267	6053	784CIP2B_377	6416
696	2482	4268	6054	784CIP2B_378	6418
697	2483	4269	6055	784CIP2B_379	6422
698	2484	4270	6056	784CIP2B_380	6423
699	2485	4271	6057	784CIP2B_381	6426
700	2486	4272	6058	784CIP2B_382	6427
701	2487	4273	6059	784CIP2B_383	6428
702	2488	4274	6060	784CIP2B_384	6429
703	2489	4275	6061	784CIP2B_385	6430
704	2490	4276	6062	784CIP2B_386	6432
705	2491	4277	6063	784CIP2B_387	6432
706	2492	4278	6064	784CIP2B_388	6438
707	2493	4279	6065	784CIP2B_389	6441
708	2494	4280	6066	784CIP2B_390	6446
709	2495	4281	6067	784CIP2B_391	6454
710	2496	4282	6068	784CIP2B_392	6459
711	2497	4283	6069	784CIP2B_394	6461
712	2498	4284	6070	784CIP2B_395	6467
713	2499	4285	6071	784CIP2B_396	6468
714	2500	4286	6072	784CIP2B_397	6487
715	2501	4287	6073	784CIP2B_398	6491
716	2502	4288	6074	784CIP2B_399	6506
717	2503	4289	6075	784CIP2B_401	6514
718	2504	4290	6076	784CIP2B_402	6519
719	2505	4291	6077	784CIP2B_403	6521
720	2506	4292	6078	784CIP2B_404	6532
721	2507	4293	6079	784CIP2B_405	6536
722	2508	4294	6080	784CIP2B_406	6543
723	2509	4295	6081	784CIP2B_407	6544
724	2510	4296	6082	784CIP2B_408	6548
725	2511	4297	6083	784CIP2B_409	6551
726	2512	4298	6084	784CIP2B_410	6551
727	2513	4299	6085	784CIP2B_411	6552
728	2514	4300	6086	784CIP2B_412	6554
729	2515	4301	6087	784CIP2B_413	6556
730	2516	4302	6088	784CIP2B_414	6560
731	2517	4303	6089	784CIP2B_415	6563
732	2518	4304	6090	784CIP2B_416	6564
733	2519	4305	6091	784CIP2B_417	6567
734	2520	4306	6092	784CIP2B_418	6573
735	2521	4307	6093	784CIP2B_419	6575
736	2522	4308	6094	784CIP2B_420	6577
737	2523	4309	6095	784CIP2B_421	6593
738	2524	4310	6096	784CIP2B_422	6595
739	2525	4311	6097	784CIP2B_423	6599
740	2526	4312	6098	784CIP2B_424	6625
741	2527	4313	6099	784CIP2B_425	6625

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
742	2528	4314	6100	784CIP2B_426	6626
743	2529	4315	6101	784CIP2B_427	6630
744	2530	4316	6102	784CIP2B_428	6631
745	2531	4317	6103	784CIP2B_429	6632
746	2532	4318	6104	784CIP2B_430	6633
747	2533	4319	6105	784CIP2B_431	6634
748	2534	4320	6106	784CIP2B_432	6638
749	2535	4321	6107	784CIP2B_433	6641
750	2536	4322	6108	784CIP2B_434	6644
751	2537	4323	6109	784CIP2B_435	6646
752	2538	4324	6110	784CIP2B_436	6648
753	2539	4325	6111	784CIP2B_437	6652
754	2540	4326	6112	784CIP2B_438	6654
755	2541	4327	6113	784CIP2B_439	6657
756	2542	4328	6114	784CIP2B_440	6658
757	2543	4329	6115	784CIP2B_441	6663
758	2544	4330	6116	784CIP2B_442	6664
759	2545	4331	6117	784CIP2B_443	6668
760	2546	4332	6118	784CIP2B_444	6669
761	2547	4333	6119	784CIP2B_445	6673
762	2548	4334	6120	784CIP2B_446	6685
763	2549	4335	6121	784CIP2B_447	6687
764	2550	4336	6122	784CIP2B_448	6689
765	2551	4337	6123	784CIP2B_449	6693
766	2552	4338	6124	784CIP2B_450	6698
767	2553	4339	6125	784CIP2B_451	6699
768	2554	4340	6126	784CIP2B_452	6705
769	2555	4341	6127	784CIP2B_453	6711
770	2556	4342	6128	784CIP2B_454	6713
771	2557	4343	6129	784CIP2B_455	6716
772	2558	4344	6130	784CIP2B_456	6725
773	2559	4345	6131	784CIP2B_457	6726
774	2560	4346	6132	784CIP2B_458	6727
775	2561	4347	6133	784CIP2B_459	6730
776	2562	4348	6134	784CIP2B_460	6730
777	2563	4349	6135	784CIP2B_461	6730
778	2564	4350	6136	784CIP2B_462	6732
779	2565	4351	6137	784CIP2B_463	6733
780	2566	4352	6138	784CIP2B_464	6737
781	2567	4353	6139	784CIP2B_465	6745
782	2568	4354	6140	784CIP2B_466	6751
783	2569	4355	6141	784CIP2B_467	6754
784	2570	4356	6142	784CIP2B_468	6758
785	2571	4357	6143	784CIP2B_469	6761
786	2572	4358	6144	784CIP2B_470	6765
787	2573	4359	6145	784CIP2B_471	6768
788	2574	4360	6146	784CIP2B_472	6773
789	2575	4361	6147	784CIP2B_473	6776
790	2576	4362	6148	784CIP2B_474	6796
791	2577	4363	6149	784CIP2B_475	6798
792	2578	4364	6150	784CIP2B_476	6823
793	2579	4365	6151	784CIP2B_477	6825
794	2580	4366	6152	784CIP2B_478	6826
795	2581	4367	6153	784CIP2B_479	6839
796	2582	4368	6154	784CIP2B_480	6844
797	2583	4369	6155	784CIP2B_482	6849
798	2584	4370	6156	784CIP2B_483	6854
799	2585	4371	6157	784CIP2B_484	6857
800	2586	4372	6158	784CIP2B_485	6861
801	2587	4373	6159	784CIP2B_486	6873
802	2588	4374	6160	784CIP2B_487	6875
803	2589	4375	6161	784CIP2B_488	6877

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
804	2590	4376	6162	784CIP2B_489	6880
805	2591	4377	6163	784CIP2B_490	6885
806	2592	4378	6164	784CIP2B_491	6890
807	2593	4379	6165	784CIP2B_492	6890
808	2594	4380	6166	784CIP2B_493	6894
809	2595	4381	6167	784CIP2B_494	6901
810	2596	4382	6168	784CIP2B_495	6904
811	2597	4383	6169	784CIP2B_496	6907
812	2598	4384	6170	784CIP2B_497	6914
813	2599	4385	6171	784CIP2B_498	6917
814	2600	4386	6172	784CIP2B_499	6923
815	2601	4387	6173	784CIP2B_500	6929
816	2602	4388	6174	784CIP2B_501	6931
817	2603	4389	6175	784CIP2B_502	6935
818	2604	4390	6176	784CIP2B_503	6940
819	2605	4391	6177	784CIP2B_504	6945
820	2606	4392	6178	784CIP2B_505	6946
821	2607	4393	6179	784CIP2B_506	6947
822	2608	4394	6180	784CIP2B_507	6949
823	2609	4395	6181	784CIP2B_508	6959
824	2610	4396	6182	784CIP2B_509	6960
825	2611	4397	6183	784CIP2B_510	6962
826	2612	4398	6184	784CIP2B_511	6963
827	2613	4399	6185	784CIP2B_512	6967
828	2614	4400	6186	784CIP2B_513	6983
829	2615	4401	6187	784CIP2B_514	6988
830	2616	4402	6188	784CIP2B_515	6996
831	2617	4403	6189	784CIP2B_516	7003
832	2618	4404	6190	784CIP2B_517	7016
833	2619	4405	6191	784CIP2B_518	7017
834	2620	4406	6192	784CIP2B_519	7025
835	2621	4407	6193	784CIP2B_520	7025
836	2622	4408	6194	784CIP2B_521	7025
837	2623	4409	6195	784CIP2B_522	7050
838	2624	4410	6196	784CIP2B_523	7051
839	2625	4411	6197	784CIP2B_524	7055
840	2626	4412	6198	784CIP2B_525	7060
841	2627	4413	6199	784CIP2B_526	7064
842	2628	4414	6200	784CIP2B_527	7067
843	2629	4415	6201	784CIP2B_528	7071
844	2630	4416	6202	784CIP2B_529	7072
845	2631	4417	6203	784CIP2B_530	7073
846	2632	4418	6204	784CIP2B_531	7076
847	2633	4419	6205	784CIP2B_532	7088
848	2634	4420	6206	784CIP2B_533	7089
849	2635	4421	6207	784CIP2B_534	7091
850	2636	4422	6208	784CIP2B_535	7091
851	2637	4423	6209	784CIP2B_536	7104
852	2638	4424	6210	784CIP2B_537	7105
853	2639	4425	6211	784CIP2B_538	7105
854	2640	4426	6212	784CIP2B_539	7109
855	2641	4427	6213	784CIP2B_540	7109
856	2642	4428	6214	784CIP2B_541	7119
857	2643	4429	6215	784CIP2B_542	7120
858	2644	4430	6216	784CIP2B_543	7121
859	2645	4431	6217	784CIP2B_544	7126
860	2646	4432	6218	784CIP2B_545	7127
861	2647	4433	6219	784CIP2B_546	7130
862	2648	4434	6220	784CIP2B_547	7131
863	2649	4435	6221	784CIP2B_548	7144
864	2650	4436	6222	784CIP2B_549	7159
865	2651	4437	6223	784CIP2B_550	7163

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
866	2652	4438	6224	784CIP2B_551	7175
867	2653	4439	6225	784CIP2B_552	7188
868	2654	4440	6226	784CIP2B_553	7189
869	2655	4441	6227	784CIP2B_554	7190
870	2656	4442	6228	784CIP2B_555	7191
871	2657	4443	6229	784CIP2B_556	7203
872	2658	4444	6230	784CIP2B_557	7204
873	2659	4445	6231	784CIP2B_558	7208
874	2660	4446	6232	784CIP2B_559	7209
875	2661	4447	6233	784CIP2B_560	7210
876	2662	4448	6234	784CIP2B_561	7216
877	2663	4449	6235	784CIP2B_562	7221
878	2664	4450	6236	784CIP2B_563	7230
879	2665	4451	6237	784CIP2B_564	7237
880	2666	4452	6238	784CIP2B_565	7240
881	2667	4453	6239	784CIP2B_566	7245
882	2668	4454	6240	784CIP2B_567	7250
883	2669	4455	6241	784CIP2B_568	7251
884	2670	4456	6242	784CIP2B_569	7255
885	2671	4457	6243	784CIP2B_570	7260
886	2672	4458	6244	784CIP2B_571	7265
887	2673	4459	6245	784CIP2B_572	7268
888	2674	4460	6246	784CIP2B_573	7275
889	2675	4461	6247	784CIP2B_574	7279
890	2676	4462	6248	784CIP2B_575	7283
891	2677	4463	6249	784CIP2B_576	7283
892	2678	4464	6250	784CIP2B_577	7287
893	2679	4465	6251	784CIP2B_578	7301
894	2680	4466	6252	784CIP2B_579	7308
895	2681	4467	6253	784CIP2B_580	7308
896	2682	4468	6254	784CIP2B_581	7309
897	2683	4469	6255	784CIP2B_582	7319
898	2684	4470	6256	784CIP2B_583	7320
899	2685	4471	6257	784CIP2B_584	7326
900	2686	4472	6258	784CIP2B_585	7326
901	2687	4473	6259	784CIP2B_586	7334
902	2688	4474	6260	784CIP2B_587	7337
903	2689	4475	6261	784CIP2B_588	7339
904	2690	4476	6262	784CIP2B_589	7344
905	2691	4477	6263	784CIP2B_590	7355
906	2692	4478	6264	784CIP2B_591	7363
907	2693	4479	6265	784CIP2B_592	7363
908	2694	4480	6266	784CIP2B_593	7365
909	2695	4481	6267	784CIP2B_594	7368
910	2696	4482	6268	784CIP2B_595	7369
911	2697	4483	6269	784CIP2B_596	7372
912	2698	4484	6270	784CIP2B_599	7375
913	2699	4485	6271	784CIP2B_600	7381
914	2700	4486	6272	784CIP2B_601	7383
915	2701	4487	6273	784CIP2B_602	7387
916	2702	4488	6274	784CIP2B_603	7391
917	2703	4489	6275	784CIP2B_604	7393
918	2704	4490	6276	784CIP2B_605	7395
919	2705	4491	6277	784CIP2B_606	7397
920	2706	4492	6278	784CIP2B_607	7399
921	2707	4493	6279	784CIP2B_608	7405
922	2708	4494	6280	784CIP2B_609	7406
923	2709	4495	6281	784CIP2B_610	7406
924	2710	4496	6282	784CIP2B_611	7409
925	2711	4497	6283	784CIP2B_612	7410
926	2712	4498	6284	784CIP2B_613	7411
927	2713	4499	6285	784CIP2B_614	7417

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
928	2714	4500	6286	784CIP2B_615	7418
929	2715	4501	6287	784CIP2B_616	7421
930	2716	4502	6288	784CIP2B_617	7422
931	2717	4503	6289	784CIP2B_618	7422
932	2718	4504	6290	784CIP2B_619	7423
933	2719	4505	6291	784CIP2B_620	7424
934	2720	4506	6292	784CIP2B_621	7426
935	2721	4507	6293	784CIP2B_622	7427
936	2722	4508	6294	784CIP2B_623	7428
937	2723	4509	6295	784CIP2B_624	7430
938	2724	4510	6296	784CIP2B_625	7435
939	2725	4511	6297	784CIP2B_626	7437
940	2726	4512	6298	784CIP2B_627	7439
941	2727	4513	6299	784CIP2B_628	7440
942	2728	4514	6300	784CIP2B_629	7442
943	2729	4515	6301	784CIP2B_630	7450
944	2730	4516	6302	784CIP2B_631	7451
945	2731	4517	6303	784CIP2B_632	7452
946	2732	4518	6304	784CIP2B_633	7454
947	2733	4519	6305	784CIP2B_634	7457
948	2734	4520	6306	784CIP2B_635	7459
949	2735	4521	6307	784CIP2B_636	7461
950	2736	4522	6308	784CIP2B_637	7463
951	2737	4523	6309	784CIP2B_638	7466
952	2738	4524	6310	784CIP2B_639	7469
953	2739	4525	6311	784CIP2B_640	7473
954	2740	4526	6312	784CIP2B_641	7481
955	2741	4527	6313	784CIP2B_642	7482
956	2742	4528	6314	784CIP2B_643	7482
957	2743	4529	6315	784CIP2B_644	7483
958	2744	4530	6316	784CIP2B_645	7485
959	2745	4531	6317	784CIP2B_646	7486
960	2746	4532	6318	784CIP2B_647	7487
961	2747	4533	6319	784CIP2B_648	7491
962	2748	4534	6320	784CIP2B_649	7492
963	2749	4535	6321	784CIP2B_650	7494
964	2750	4536	6322	784CIP2B_651	7498
965	2751	4537	6323	784CIP2B_652	7504
966	2752	4538	6324	784CIP2B_653	7508
967	2753	4539	6325	784CIP2B_654	7516
968	2754	4540	6326	784CIP2B_655	7518
969	2755	4541	6327	784CIP2B_656	7519
970	2756	4542	6328	784CIP2B_657	7521
971	2757	4543	6329	784CIP2B_658	7529
972	2758	4544	6330	784CIP2B_659	7532
973	2759	4545	6331	784CIP2B_660	7533
974	2760	4546	6332	784CIP2B_661	7535
975	2761	4547	6333	784CIP2B_662	7545
976	2762	4548	6334	784CIP2B_663	7546
977	2763	4549	6335	784CIP2B_664	7552
978	2764	4550	6336	784CIP2B_665	7554
979	2765	4551	6337	784CIP2B_666	7567
980	2766	4552	6338	784CIP2B_667	7569
981	2767	4553	6339	784CIP2B_668	7575
982	2768	4554	6340	784CIP2B_669	7576
983	2769	4555	6341	784CIP2B_670	7577
984	2770	4556	6342	784CIP2B_671	7579
985	2771	4557	6343	784CIP2B_672	7582
986	2772	4558	6344	784CIP2B_673	7587
987	2773	4559	6345	784CIP2B_674	7589
988	2774	4560	6346	784CIP2B_675	7597
989	2775	4561	6347	784CIP2B_676	7597

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
990	2776	4562	6348	784CIP2B_677	7609
991	2777	4563	6349	784CIP2B_678	7609
992	2778	4564	6350	784CIP2B_679	7609
993	2779	4565	6351	784CIP2B_680	7613
994	2780	4566	6352	784CIP2B_681	7623
995	2781	4567	6353	784CIP2B_682	7629
996	2782	4568	6354	784CIP2B_683	7630
997	2783	4569	6355	784CIP2B_684	7633
998	2784	4570	6356	784CIP2B_685	7635
999	2785	4571	6357	784CIP2B_686	7638
1000	2786	4572	6358	784CIP2B_687	7639
1001	2787	4573	6359	784CIP2B_688	7646
1002	2788	4574	6360	784CIP2B_689	7647
1003	2789	4575	6361	784CIP2B_690	7648
1004	2790	4576	6362	784CIP2B_691	7658
1005	2791	4577	6363	784CIP2B_692	7664
1006	2792	4578	6364	784CIP2B_693	7664
1007	2793	4579	6365	784CIP2B_695	7674
1008	2794	4580	6366	784CIP2B_696	7675
1009	2795	4581	6367	784CIP2B_697	7676
1010	2796	4582	6368	784CIP2B_698	7681
1011	2797	4583	6369	784CIP2B_699	7688
1012	2798	4584	6370	784CIP2B_700	7693
1013	2799	4585	6371	784CIP2B_701	7694
1014	2800	4586	6372	784CIP2B_702	7715
1015	2801	4587	6373	784CIP2B_703	7716
1016	2802	4588	6374	784CIP2B_704	7718
1017	2803	4589	6375	784CIP2B_705	7721
1018	2804	4590	6376	784CIP2B_706	7723
1019	2805	4591	6377	784CIP2B_707	7729
1020	2806	4592	6378	784CIP2B_708	7733
1021	2807	4593	6379	784CIP2B_709	7735
1022	2808	4594	6380	784CIP2B_710	7741
1023	2809	4595	6381	784CIP2B_711	7743
1024	2810	4596	6382	784CIP2B_712	7748
1025	2811	4597	6383	784CIP2B_713	7749
1026	2812	4598	6384	784CIP2B_714	7750
1027	2813	4599	6385	784CIP2B_715	7757
1028	2814	4600	6386	784CIP2B_716	7759
1029	2815	4601	6387	784CIP2B_717	7760
1030	2816	4602	6388	784CIP2B_718	7760
1031	2817	4603	6389	784CIP2B_719	7764
1032	2818	4604	6390	784CIP2B_720	7765
1033	2819	4605	6391	784CIP2B_721	7766
1034	2820	4606	6392	784CIP2B_722	7767
1035	2821	4607	6393	784CIP2B_723	7769
1036	2822	4608	6394	784CIP2B_724	7770
1037	2823	4609	6395	784CIP2B_725	7774
1038	2824	4610	6396	784CIP2B_726	7779
1039	2825	4611	6397	784CIP2B_727	7781
1040	2826	4612	6398	784CIP2B_728	7782
1041	2827	4613	6399	784CIP2B_729	7783
1042	2828	4614	6400	784CIP2B_730	7787
1043	2829	4615	6401	784CIP2B_731	7792
1044	2830	4616	6402	784CIP2B_732	7795
1045	2831	4617	6403	784CIP2B_733	7801
1046	2832	4618	6404	784CIP2B_734	7807
1047	2833	4619	6405	784CIP2B_735	7808
1048	2834	4620	6406	784CIP2B_736	7819
1049	2835	4621	6407	784CIP2B_737	7824
1050	2836	4622	6408	784CIP2B_738	7826
1051	2837	4623	6409	784CIP2B_739	7829

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1052	2838	4624	6410	784CIP2B_740	7832
1053	2839	4625	6411	784CIP2B_741	7839
1054	2840	4626	6412	784CIP2B_743	7847
1055	2841	4627	6413	784CIP2B_744	7848
1056	2842	4628	6414	784CIP2B_745	7853
1057	2843	4629	6415	784CIP2B_746	7854
1058	2844	4630	6416	784CIP2B_747	7856
1059	2845	4631	6417	784CIP2B_748	7862
1060	2846	4632	6418	784CIP2B_749	7865
1061	2847	4633	6419	784CIP2B_750	7874
1062	2848	4634	6420	784CIP2B_751	7877
1063	2849	4635	6421	784CIP2B_752	7880
1064	2850	4636	6422	784CIP2B_753	7882
1065	2851	4637	6423	784CIP2B_754	7884
1066	2852	4638	6424	784CIP2B_755	7886
1067	2853	4639	6425	784CIP2B_756	7888
1068	2854	4640	6426	784CIP2B_757	7889
1069	2855	4641	6427	784CIP2B_758	7901
1070	2856	4642	6428	784CIP2B_759	7910
1071	2857	4643	6429	784CIP2B_760	7911
1072	2858	4644	6430	784CIP2B_761	7921
1073	2859	4645	6431	784CIP2B_762	7923
1074	2860	4646	6432	784CIP2B_763	7924
1075	2861	4647	6433	784CIP2B_764	7925
1076	2862	4648	6434	784CIP2B_765	7928
1077	2863	4649	6435	784CIP2B_766	7929
1078	2864	4650	6436	784CIP2B_767	7930
1079	2865	4651	6437	784CIP2B_768	7934
1080	2866	4652	6438	784CIP2B_769	7938
1081	2867	4653	6439	784CIP2B_770	7942
1082	2868	4654	6440	784CIP2B_771	7945
1083	2869	4655	6441	784CIP2B_772	7946
1084	2870	4656	6442	784CIP2B_773	7948
1085	2871	4657	6443	784CIP2B_774	7951
1086	2872	4658	6444	784CIP2B_775	7952
1087	2873	4659	6445	784CIP2B_776	7953
1088	2874	4660	6446	784CIP2B_777	7954
1089	2875	4661	6447	784CIP2B_778	7957
1090	2876	4662	6448	784CIP2B_779	7958
1091	2877	4663	6449	784CIP2B_780	7961
1092	2878	4664	6450	784CIP2B_781	7965
1093	2879	4665	6451	784CIP2B_782	7966
1094	2880	4666	6452	784CIP2B_783	7979
1095	2881	4667	6453	784CIP2B_784	7986
1096	2882	4668	6454	784CIP2B_785	7988
1097	2883	4669	6455	784CIP2B_786	7988
1098	2884	4670	6456	784CIP2B_787	7991
1099	2885	4671	6457	784CIP2B_788	7992
1100	2886	4672	6458	784CIP2B_789	7992
1101	2887	4673	6459	784CIP2B_790	7992
1102	2888	4674	6460	784CIP2B_791	7992
1103	2889	4675	6461	784CIP2B_792	8003
1104	2890	4676	6462	784CIP2B_793	8014
1105	2891	4677	6463	784CIP2B_794	8015
1106	2892	4678	6464	784CIP2B_795	8016
1107	2893	4679	6465	784CIP2B_796	8017
1108	2894	4680	6466	784CIP2B_797	8019
1109	2895	4681	6467	784CIP2B_798	8020
1110	2896	4682	6468	784CIP2B_799	8022
1111	2897	4683	6469	784CIP2B_800	8022
1112	2898	4684	6470	784CIP2B_801	8028
1113	2899	4685	6471	784CIP2B_802	8030

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1114	2900	4686	6472	784CIP2B_803	8038
1115	2901	4687	6473	784CIP2B_804	8042
1116	2902	4688	6474	784CIP2B_805	8045
1117	2903	4689	6475	784CIP2B_806	8045
1118	2904	4690	6476	784CIP2B_807	8046
1119	2905	4691	6477	784CIP2B_808	8047
1120	2906	4692	6478	784CIP2B_809	8051
1121	2907	4693	6479	784CIP2B_810	8059
1122	2908	4694	6480	784CIP2B_811	8064
1123	2909	4695	6481	784CIP2B_812	8069
1124	2910	4696	6482	784CIP2B_813	8074
1125	2911	4697	6483	784CIP2B_814	8077
1126	2912	4698	6484	784CIP2B_815	8078
1127	2913	4699	6485	784CIP2B_816	8079
1128	2914	4700	6486	784CIP2B_817	8084
1129	2915	4701	6487	784CIP2B_818	8088
1130	2916	4702	6488	784CIP2B_819	8090
1131	2917	4703	6489	784CIP2B_820	8091
1132	2918	4704	6490	784CIP2B_821	8099
1133	2919	4705	6491	784CIP2B_822	8099
1134	2920	4706	6492	784CIP2B_823	8100
1135	2921	4707	6493	784CIP2B_824	8102
1136	2922	4708	6494	784CIP2B_825	8103
1137	2923	4709	6495	784CIP2B_826	8103
1138	2924	4710	6496	784CIP2B_827	8104
1139	2925	4711	6497	784CIP2B_828	8108
1140	2926	4712	6498	784CIP2B_829	8110
1141	2927	4713	6499	784CIP2B_830	8116
1142	2928	4714	6500	784CIP2B_831	8117
1143	2929	4715	6501	784CIP2B_832	8123
1144	2930	4716	6502	784CIP2B_833	8130
1145	2931	4717	6503	784CIP2B_834	8130
1146	2932	4718	6504	784CIP2B_835	8143
1147	2933	4719	6505	784CIP2B_836	8143
1148	2934	4720	6506	784CIP2B_837	8154
1149	2935	4721	6507	784CIP2B_838	8155
1150	2936	4722	6508	784CIP2B_839	8162
1151	2937	4723	6509	784CIP2B_840	8163
1152	2938	4724	6510	784CIP2B_841	8172
1153	2939	4725	6511	784CIP2B_842	8173
1154	2940	4726	6512	784CIP2B_843	8179
1155	2941	4727	6513	784CIP2B_844	8182
1156	2942	4728	6514	784CIP2B_845	8183
1157	2943	4729	6515	784CIP2B_846	8184
1158	2944	4730	6516	784CIP2B_847	8185
1159	2945	4731	6517	784CIP2B_848	8187
1160	2946	4732	6518	784CIP2B_849	8188
1161	2947	4733	6519	784CIP2B_850	8190
1162	2948	4734	6520	784CIP2B_851	8190
1163	2949	4735	6521	784CIP2B_852	8192
1164	2950	4736	6522	784CIP2B_853	8193
1165	2951	4737	6523	784CIP2B_854	8197
1166	2952	4738	6524	784CIP2B_855	8197
1167	2953	4739	6525	784CIP2B_856	8199
1168	2954	4740	6526	784CIP2B_857	8202
1169	2955	4741	6527	784CIP2B_858	8203
1170	2956	4742	6528	784CIP2B_859	8208
1171	2957	4743	6529	784CIP2B_860	8209
1172	2958	4744	6530	784CIP2B_861	8211
1173	2959	4745	6531	784CIP2B_862	8214
1174	2960	4746	6532	784CIP2B_863	8217
1175	2961	4747	6533	784CIP2B_864	8223

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1176	2962	4748	6534	784CIP2B_865	8224
1177	2963	4749	6535	784CIP2B_866	8226
1178	2964	4750	6536	784CIP2B_867	8227
1179	2965	4751	6537	784CIP2B_868	8229
1180	2966	4752	6538	784CIP2B_869	8232
1181	2967	4753	6539	784CIP2B_870	8236
1182	2968	4754	6540	784CIP2B_871	8239
1183	2969	4755	6541	784CIP2B_872	8244
1184	2970	4756	6542	784CIP2B_873	8245
1185	2971	4757	6543	784CIP2B_874	8248
1186	2972	4758	6544	784CIP2B_875	8251
1187	2973	4759	6545	784CIP2B_876	8253
1188	2974	4760	6546	784CIP2B_877	8260
1189	2975	4761	6547	784CIP2B_878	8262
1190	2976	4762	6548	784CIP2B_879	8268
1191	2977	4763	6549	784CIP2B_880	8270
1192	2978	4764	6550	784CIP2B_881	8272
1193	2979	4765	6551	784CIP2B_882	8274
1194	2980	4766	6552	784CIP2B_883	8274
1195	2981	4767	6553	784CIP2B_884	8275
1196	2982	4768	6554	784CIP2B_885	8277
1197	2983	4769	6555	784CIP2B_886	8281
1198	2984	4770	6556	784CIP2B_887	8283
1199	2985	4771	6557	784CIP2B_888	8289
1200	2986	4772	6558	784CIP2B_889	8295
1201	2987	4773	6559	784CIP2B_890	8300
1202	2988	4774	6560	784CIP2B_891	8303
1203	2989	4775	6561	784CIP2B_892	8304
1204	2990	4776	6562	784CIP2B_893	8305
1205	2991	4777	6563	784CIP2B_894	8309
1206	2992	4778	6564	784CIP2B_895	8318
1207	2993	4779	6565	784CIP2B_896	8319
1208	2994	4780	6566	784CIP2B_897	8321
1209	2995	4781	6567	784CIP2B_898	8322
1210	2996	4782	6568	784CIP2B_899	8323
1211	2997	4783	6569	784CIP2B_900	8325
1212	2998	4784	6570	784CIP2B_901	8331
1213	2999	4785	6571	784CIP2B_902	8332
1214	3000	4786	6572	784CIP2B_903	8333
1215	3001	4787	6573	784CIP2B_904	8335
1216	3002	4788	6574	784CIP2B_905	8336
1217	3003	4789	6575	784CIP2B_906	8337
1218	3004	4790	6576	784CIP2B_907	8340
1219	3005	4791	6577	784CIP2B_908	8343
1220	3006	4792	6578	784CIP2B_909	8347
1221	3007	4793	6579	784CIP2B_910	8349
1222	3008	4794	6580	784CIP2B_911	8351
1223	3009	4795	6581	784CIP2B_912	8353
1224	3010	4796	6582	784CIP2B_913	8355
1225	3011	4797	6583	784CIP2B_914	8361
1226	3012	4798	6584	784CIP2B_915	8365
1227	3013	4799	6585	784CIP2B_916	8367
1228	3014	4800	6586	784CIP2B_917	8369
1229	3015	4801	6587	784CIP2B_919	8375
1230	3016	4802	6588	784CIP2B_920	8387
1231	3017	4803	6589	784CIP2B_921	8391
1232	3018	4804	6590	784CIP2B_922	8393
1233	3019	4805	6591	784CIP2B_923	8393
1234	3020	4806	6592	784CIP2B_924	8394
1235	3021	4807	6593	784CIP2B_925	8395
1236	3022	4808	6594	784CIP2B_926	8396
1237	3023	4809	6595	784CIP2B_927	8398

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1238	3024	4810	6596	784CIP2B_928	8402
1239	3025	4811	6597	784CIP2B_929	8402
1240	3026	4812	6598	784CIP2B_930	8405
1241	3027	4813	6599	784CIP2B_931	8406
1242	3028	4814	6600	784CIP2B_932	8409
1243	3029	4815	6601	784CIP2B_933	8410
1244	3030	4816	6602	784CIP2B_934	8414
1245	3031	4817	6603	784CIP2B_935	8415
1246	3032	4818	6604	784CIP2B_936	8419
1247	3033	4819	6605	784CIP2B_937	8426
1248	3034	4820	6606	784CIP2B_938	8430
1249	3035	4821	6607	784CIP2B_939	8431
1250	3036	4822	6608	784CIP2B_940	8432
1251	3037	4823	6609	784CIP2B_941	8433
1252	3038	4824	6610	784CIP2B_942	8434
1253	3039	4825	6611	784CIP2B_943	8438
1254	3040	4826	6612	784CIP2B_944	8439
1255	3041	4827	6613	784CIP2B_945	8441
1256	3042	4828	6614	784CIP2B_946	8450
1257	3043	4829	6615	784CIP2B_947	8451
1258	3044	4830	6616	784CIP2B_948	8452
1259	3045	4831	6617	784CIP2B_949	8460
1260	3046	4832	6618	784CIP2B_950	8461
1261	3047	4833	6619	784CIP2B_951	8462
1262	3048	4834	6620	784CIP2B_952	8464
1263	3049	4835	6621	784CIP2B_953	8465
1264	3050	4836	6622	784CIP2B_954	8467
1265	3051	4837	6623	784CIP2B_955	8470
1266	3052	4838	6624	784CIP2B_956	8471
1267	3053	4839	6625	784CIP2B_957	8473
1268	3054	4840	6626	784CIP2B_958	8474
1269	3055	4841	6627	784CIP2B_959	8475
1270	3056	4842	6628	784CIP2B_960	8476
1271	3057	4843	6629	784CIP2B_961	8480
1272	3058	4844	6630	784CIP2B_962	8482
1273	3059	4845	6631	784CIP2B_963	8482
1274	3060	4846	6632	784CIP2B_964	8486
1275	3061	4847	6633	784CIP2B_965	8488
1276	3062	4848	6634	784CIP2B_966	8492
1277	3063	4849	6635	784CIP2B_967	8494
1278	3064	4850	6636	784CIP2B_968	8496
1279	3065	4851	6637	784CIP2B_969	8497
1280	3066	4852	6638	784CIP2B_970	8499
1281	3067	4853	6639	784CIP2B_971	8513
1282	3068	4854	6640	784CIP2B_972	8522
1283	3069	4855	6641	784CIP2B_973	8526
1284	3070	4856	6642	784CIP2B_974	8531
1285	3071	4857	6643	784CIP2B_975	8533
1286	3072	4858	6644	784CIP2B_976	8542
1287	3073	4859	6645	784CIP2B_977	8544
1288	3074	4860	6646	784CIP2B_978	8565
1289	3075	4861	6647	784CIP2B_979	8565
1290	3076	4862	6648	784CIP2B_980	8572
1291	3077	4863	6649	784CIP2B_981	8576
1292	3078	4864	6650	784CIP2B_982	8578
1293	3079	4865	6651	784CIP2B_983	8584
1294	3080	4866	6652	784CIP2B_984	8598
1295	3081	4867	6653	784CIP2B_985	8602
1296	3082	4868	6654	784CIP2B_986	8604
1297	3083	4869	6655	784CIP2B_987	8609
1298	3084	4870	6656	784CIP2B_988	8612
1299	3085	4871	6657	784CIP2B_989	8637

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1300	3086	4872	6658	784CIP2B_990	8640
1301	3087	4873	6659	784CIP2B_991	8643
1302	3088	4874	6660	784CIP2B_992	8645
1303	3089	4875	6661	784CIP2B_993	8650
1304	3090	4876	6662	784CIP2B_994	8651
1305	3091	4877	6663	784CIP2B_995	8654
1306	3092	4878	6664	784CIP2B_996	8655
1307	3093	4879	6665	784CIP2B_997	8657
1308	3094	4880	6666	784CIP2B_998	8665
1309	3095	4881	6667	784CIP2B_999	8668
1310	3096	4882	6668	784CIP2B_1000	8671
1311	3097	4883	6669	784CIP2B_1001	8672
1312	3098	4884	6670	784CIP2B_1002	8692
1313	3099	4885	6671	784CIP2B_1003	8706
1314	3100	4886	6672	784CIP2B_1004	8716
1315	3101	4887	6673	784CIP2B_1005	8719
1316	3102	4888	6674	784CIP2B_1006	8743
1317	3103	4889	6675	784CIP2B_1007	8764
1318	3104	4890	6676	784CIP2B_1008	8764
1319	3105	4891	6677	784CIP2B_1009	8764
1320	3106	4892	6678	784CIP2B_1010	8774
1321	3107	4893	6679	784CIP2B_1011	8782
1322	3108	4894	6680	784CIP2B_1012	8796
1323	3109	4895	6681	784CIP2B_1013	8827
1324	3110	4896	6682	784CIP2B_1014	8842
1325	3111	4897	6683	784CIP2B_1015	8842
1326	3112	4898	6684	784CIP2B_1016	8858
1327	3113	4899	6685	784CIP2B_1017	8871
1328	3114	4900	6686	784CIP2B_1018	8921
1329	3115	4901	6687	784CIP2B_1019	8927
1330	3116	4902	6688	784CIP2B_1020	8942
1331	3117	4903	6689	784CIP2B_1021	8994
1332	3118	4904	6690	784CIP2B_1022	9023
1333	3119	4905	6691	784CIP2B_1023	9028
1334	3120	4906	6692	784CIP2B_1024	9058
1335	3121	4907	6693	784CIP2B_1025	9058
1336	3122	4908	6694	784CIP2B_1026	9079
1337	3123	4909	6695	784CIP2B_1027	9079
1338	3124	4910	6696	784CIP2B_1028	9082
1339	3125	4911	6697	784CIP2B_1029	9084
1340	3126	4912	6698	784CIP2B_1030	9093
1341	3127	4913	6699	784CIP2B_1031	9101
1342	3128	4914	6700	784CIP2B_1032	9103
1343	3129	4915	6701	784CIP2B_1033	9105
1344	3130	4916	6702	784CIP2B_1034	9151
1345	3131	4917	6703	784CIP2B_1035	9161
1346	3132	4918	6704	784CIP2B_1036	9172
1347	3133	4919	6705	784CIP2B_1037	9174
1348	3134	4920	6706	784CIP2B_1038	9204
1349	3135	4921	6707	784CIP2B_1039	9234
1350	3136	4922	6708	784CIP2B_1040	9235
1351	3137	4923	6709	784CIP2B_1041	9239
1352	3138	4924	6710	784CIP2B_1042	9256
1353	3139	4925	6711	784CIP2B_1043	9276
1354	3140	4926	6712	784CIP2B_1044	9345
1355	3141	4927	6713	784CIP2B_1045	9379
1356	3142	4928	6714	784CIP2B_1046	9435
1357	3143	4929	6715	784CIP2B_1047	9437
1358	3144	4930	6716	784CIP2B_1048	9469
1359	3145	4931	6717	784CIP2B_1049	9500
1360	3146	4932	6718	784CIP2B_1050	9502
1361	3147	4933	6719	784CIP2B_1051	9520

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1362	3148	4934	6720	784CIP2B_1052	9541
1363	3149	4935	6721	784CIP2B_1053	9541
1364	3150	4936	6722	784CIP2B_1054	9548
1365	3151	4937	6723	784CIP2B_1055	9556
1366	3152	4938	6724	784CIP2B_1056	9556
1367	3153	4939	6725	784CIP2B_1057	9575
1368	3154	4940	6726	784CIP2B_1058	9589
1369	3155	4941	6727	784CIP2B_1059	9599
1370	3156	4942	6728	784CIP2B_1060	9602
1371	3157	4943	6729	784CIP2B_1061	9606
1372	3158	4944	6730	784CIP2B_1062	9622
1373	3159	4945	6731	784CIP2B_1063	9623
1374	3160	4946	6732	784CIP2B_1064	9646
1375	3161	4947	6733	784CIP2B_1065	9747
1376	3162	4948	6734	784CIP2B_1066	9773
1377	3163	4949	6735	784CIP2B_1067	9785
1378	3164	4950	6736	784CIP2B_1068	9801
1379	3165	4951	6737	784CIP2B_1069	9811
1380	3166	4952	6738	784CIP2B_1070	9843
1381	3167	4953	6739	784CIP2B_1071	9854
1382	3168	4954	6740	784CIP2B_1072	9854
1383	3169	4955	6741	784CIP2B_1073	9864
1384	3170	4956	6742	784CIP2B_1074	9864
1385	3171	4957	6743	784CIP2B_1075	9871
1386	3172	4958	6744	784CIP2B_1076	9879
1387	3173	4959	6745	784CIP2B_1077	9881
1388	3174	4960	6746	784CIP2B_1078	9885
1389	3175	4961	6747	784CIP2B_1079	9901
1390	3176	4962	6748	784CIP2B_1080	9912
1391	3177	4963	6749	784CIP2B_1081	9916
1392	3178	4964	6750	784CIP2B_1082	9921
1393	3179	4965	6751	784CIP2B_1083	9925
1394	3180	4966	6752	784CIP2B_1084	9930
1395	3181	4967	6753	784CIP2B_1085	9949
1396	3182	4968	6754	784CIP2B_1086	9951
1397	3183	4969	6755	784CIP2B_1087	9959
1398	3184	4970	6756	784CIP2B_1088	9973
1399	3185	4971	6757	784CIP2B_1089	9982
1400	3186	4972	6758	784CIP2B_1090	9994
1401	3187	4973	6759	784CIP2B_1091	10021
1402	3188	4974	6760	784CIP2B_1092	10041
1403	3189	4975	6761	784CIP2B_1094	10067
1404	3190	4976	6762	784CIP2B_1095	10073
1405	3191	4977	6763	784CIP2B_1096	10112
1406	3192	4978	6764	784CIP2B_1097	10117
1407	3193	4979	6765	784CIP2B_1098	10132
1408	3194	4980	6766	784CIP2B_1099	10169
1409	3195	4981	6767	784CIP2B_1100	10217
1410	3196	4982	6768	784CIP2B_1101	10226
1411	3197	4983	6769	784CIP2B_1102	10232
1412	3198	4984	6770	784CIP2B_1103	10237
1413	3199	4985	6771	784CIP2B_1104	10279
1414	3200	4986	6772	784CIP2C_1	33
1415	3201	4987	6773	784CIP2C_2	271
1416	3202	4988	6774	784CIP2C_3	848
1417	3203	4989	6775	784CIP2C_4	849
1418	3204	4990	6776	784CIP2C_5	864
1419	3205	4991	6777	784CIP2C_6	953
1420	3206	4992	6778	784CIP2C_7	980
1421	3207	4993	6779	784CIP2C_8	1595
1422	3208	4994	6780	784CIP2C_9	1697
1423	3209	4995	6781	784CIP2C_10	1744

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1424	3210	4996	6782	784CIP2C_11	1937
1425	3211	4997	6783	784CIP2C_12	1955
1426	3212	4998	6784	784CIP2C_13	1955
1427	3213	4999	6785	784CIP2C_14	2185
1428	3214	5000	6786	784CIP2C_15	2889
1429	3215	5001	6787	784CIP2C_16	2901
1430	3216	5002	6788	784CIP2C_17	2902
1431	3217	5003	6789	784CIP2C_18	2905
1432	3218	5004	6790	784CIP2C_19	2948
1433	3219	5005	6791	784CIP2C_20	2956
1434	3220	5006	6792	784CIP2C_21	2959
1435	3221	5007	6793	784CIP2C_22	2965
1436	3222	5008	6794	784CIP2C_23	2966
1437	3223	5009	6795	784CIP2C_24	2970
1438	3224	5010	6796	784CIP2C_25	2985
1439	3225	5011	6797	784CIP2C_26	2987
1440	3226	5012	6798	784CIP2C_27	2993
1441	3227	5013	6799	784CIP2C_28	2993
1442	3228	5014	6800	784CIP2C_29	3017
1443	3229	5015	6801	784CIP2C_30	3046
1444	3230	5016	6802	784CIP2C_31	3050
1445	3231	5017	6803	784CIP2C_32	3357
1446	3232	5018	6804	784CIP2C_33	3359
1447	3233	5019	6805	784CIP2C_34	3432
1448	3234	5020	6806	784CIP2C_35	3438
1449	3235	5021	6807	784CIP2C_36	3439
1450	3236	5022	6808	784CIP2C_39	3463
1451	3237	5023	6809	784CIP2C_40	3466
1452	3238	5024	6810	784CIP2C_41	3466
1453	3239	5025	6811	784CIP2C_42	3467
1454	3240	5026	6812	784CIP2C_43	3468
1455	3241	5027	6813	784CIP2C_44	3483
1456	3242	5028	6814	784CIP2C_45	3484
1457	3243	5029	6815	784CIP2C_46	3488
1458	3244	5030	6816	784CIP2C_47	3491
1459	3245	5031	6817	784CIP2C_48	3493
1460	3246	5032	6818	784CIP2C_49	3494
1461	3247	5033	6819	784CIP2C_50	3495
1462	3248	5034	6820	784CIP2C_51	3496
1463	3249	5035	6821	784CIP2C_52	3503
1464	3250	5036	6822	784CIP2C_53	3503
1465	3251	5037	6823	784CIP2C_54	3504
1466	3252	5038	6824	784CIP2C_55	3511
1467	3253	5039	6825	784CIP2C_56	3531
1468	3254	5040	6826	784CIP2C_57	3536
1469	3255	5041	6827	784CIP2C_58	3546
1470	3256	5042	6828	784CIP2C_59	3548
1471	3257	5043	6829	784CIP2C_60	3551
1472	3258	5044	6830	784CIP2C_61	3553
1473	3259	5045	6831	784CIP2C_62	3564
1474	3260	5046	6832	784CIP2C_63	3567
1475	3261	5047	6833	784CIP2C_64	3572
1476	3262	5048	6834	784CIP2C_65	3573
1477	3263	5049	6835	784CIP2C_66	3574
1478	3264	5050	6836	784CIP2C_67	3583
1479	3265	5051	6837	784CIP2C_68	3615
1480	3266	5052	6838	784CIP2C_69	3623
1481	3267	5053	6839	784CIP2C_70	3629
1482	3268	5054	6840	784CIP2C_71	3666
1483	3269	5055	6841	784CIP2C_72	3667
1484	3270	5056	6842	784CIP2C_73	3906
1485	3271	5057	6843	784CIP2C_74	3912

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1486	3272	5058	6844	784CIP2C_75	3924
1487	3273	5059	6845	784CIP2C_76	3928
1488	3274	5060	6846	784CIP2C_77	3935
1489	3275	5061	6847	784CIP2C_78	3959
1490	3276	5062	6848	784CIP2C_79	3981
1491	3277	5063	6849	784CIP2C_80	3989
1492	3278	5064	6850	784CIP2C_81	4295
1493	3279	5065	6851	784CIP2C_82	4300
1494	3280	5066	6852	784CIP2C_83	4360
1495	3281	5067	6853	784CIP2C_84	4362
1496	3282	5068	6854	784CIP2C_85	4371
1497	3283	5069	6855	784CIP2C_86	4373
1498	3284	5070	6856	784CIP2C_87	4376
1499	3285	5071	6857	784CIP2C_89	4378
1500	3286	5072	6858	784CIP2C_90	4382
1501	3287	5073	6859	784CIP2C_91	4409
1502	3288	5074	6860	784CIP2C_92	4421
1503	3289	5075	6861	784CIP2C_93	4421
1504	3290	5076	6862	784CIP2C_94	4426
1505	3291	5077	6863	784CIP2C_95	4430
1506	3292	5078	6864	784CIP2C_96	4435
1507	3293	5079	6865	784CIP2C_97	4436
1508	3294	5080	6866	784CIP2C_98	4439
1509	3295	5081	6867	784CIP2C_99	4440
1510	3296	5082	6868	784CIP2C_100	4441
1511	3297	5083	6869	784CIP2C_101	4442
1512	3298	5084	6870	784CIP2C_102	4455
1513	3299	5085	6871	784CIP2C_103	4462
1514	3300	5086	6872	784CIP2C_104	4466
1515	3301	5087	6873	784CIP2C_105	4469
1516	3302	5088	6874	784CIP2C_106	4477
1517	3303	5089	6875	784CIP2C_107	4481
1518	3304	5090	6876	784CIP2C_108	4483
1519	3305	5091	6877	784CIP2C_109	4484
1520	3306	5092	6878	784CIP2C_110	4486
1521	3307	5093	6879	784CIP2C_111	4490
1522	3308	5094	6880	784CIP2C_112	4499
1523	3309	5095	6881	784CIP2C_113	4503
1524	3310	5096	6882	784CIP2C_114	4506
1525	3311	5097	6883	784CIP2C_115	4509
1526	3312	5098	6884	784CIP2C_116	4514
1527	3313	5099	6885	784CIP2C_117	4516
1528	3314	5100	6886	784CIP2C_118	4522
1529	3315	5101	6887	784CIP2C_119	4525
1530	3316	5102	6888	784CIP2C_120	4527
1531	3317	5103	6889	784CIP2C_121	4528
1532	3318	5104	6890	784CIP2C_122	4529
1533	3319	5105	6891	784CIP2C_123	4532
1534	3320	5106	6892	784CIP2C_124	4537
1535	3321	5107	6893	784CIP2C_125	4538
1536	3322	5108	6894	784CIP2C_126	4551
1537	3323	5109	6895	784CIP2C_127	4552
1538	3324	5110	6896	784CIP2C_128	4559
1539	3325	5111	6897	784CIP2C_129	4567
1540	3326	5112	6898	784CIP2C_130	4568
1541	3327	5113	6899	784CIP2C_132	4585
1542	3328	5114	6900	784CIP2C_133	4592
1543	3329	5115	6901	784CIP2C_134	4609
1544	3330	5116	6902	784CIP2C_135	4616
1545	3331	5117	6903	784CIP2C_136	4617
1546	3332	5118	6904	784CIP2C_137	4618
1547	3333	5119	6905	784CIP2C_138	4620

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1548	3334	5120	6906	784CIP2C_139	4624
1549	3335	5121	6907	784CIP2C_140	4632
1550	3336	5122	6908	784CIP2C_141	4634
1551	3337	5123	6909	784CIP2C_142	4638
1552	3338	5124	6910	784CIP2C_143	4639
1553	3339	5125	6911	784CIP2C_144	4643
1554	3340	5126	6912	784CIP2C_145	4644
1555	3341	5127	6913	784CIP2C_146	4655
1556	3342	5128	6914	784CIP2C_147	4660
1557	3343	5129	6915	784CIP2C_148	4677
1558	3344	5130	6916	784CIP2C_149	4677
1559	3345	5131	6917	784CIP2C_150	4677
1560	3346	5132	6918	784CIP2C_152	4682
1561	3347	5133	6919	784CIP2C_153	4690
1562	3348	5134	6920	784CIP2C_154	4691
1563	3349	5135	6921	784CIP2C_155	4727
1564	3350	5136	6922	784CIP2C_156	4730
1565	3351	5137	6923	784CIP2C_157	4734
1566	3352	5138	6924	784CIP2C_158	4757
1567	3353	5139	6925	784CIP2C_159	4764
1568	3354	5140	6926	784CIP2C_160	4786
1569	3355	5141	6927	784CIP2C_161	4793
1570	3356	5142	6928	784CIP2C_162	4825
1571	3357	5143	6929	784CIP2C_163	4826
1572	3358	5144	6930	784CIP2C_164	4850
1573	3359	5145	6931	784CIP2C_165	4853
1574	3360	5146	6932	784CIP2C_166	4855
1575	3361	5147	6933	784CIP2C_167	4856
1576	3362	5148	6934	784CIP2C_168	4867
1577	3363	5149	6935	784CIP2C_169	4869
1578	3364	5150	6936	784CIP2C_170	4878
1579	3365	5151	6937	784CIP2C_171	4880
1580	3366	5152	6938	784CIP2C_172	4942
1581	3367	5153	6939	784CIP2C_173	4945
1582	3368	5154	6940	784CIP2C_174	4950
1583	3369	5155	6941	784CIP2C_175	4952
1584	3370	5156	6942	784CIP2C_176	4954
1585	3371	5157	6943	784CIP2C_177	4958
1586	3372	5158	6944	784CIP2C_178	4961
1587	3373	5159	6945	784CIP2C_179	5590
1588	3374	5160	6946	784CIP2C_180	5689
1589	3375	5161	6947	784CIP2C_181	5692
1590	3376	5162	6948	784CIP2C_182	5732
1591	3377	5163	6949	784CIP2C_183	5765
1592	3378	5164	6950	784CIP2C_184	5771
1593	3379	5165	6951	784CIP2C_185	5774
1594	3380	5166	6952	784CIP2C_186	5793
1595	3381	5167	6953	784CIP2C_187	5806
1596	3382	5168	6954	784CIP2C_188	5852
1597	3383	5169	6955	784CIP2C_189	5892
1598	3384	5170	6956	784CIP2C_190	6057
1599	3385	5171	6957	784CIP2C_191	6061
1600	3386	5172	6958	784CIP2C_192	6109
1601	3387	5173	6959	784CIP2C_193	6160
1602	3388	5174	6960	784CIP2C_194	6297
1603	3389	5175	6961	784CIP2C_195	6398
1604	3390	5176	6962	784CIP2C_196	6398
1605	3391	5177	6963	784CIP2C_197	6415
1606	3392	5178	6964	784CIP2C_198	6448
1607	3393	5179	6965	784CIP2C_199	6469
1608	3394	5180	6966	784CIP2C_200	6476
1609	3395	5181	6967	784CIP2C_201	6561

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1610	3396	5182	6968	784CIP2C_202	6574
1611	3397	5183	6969	784CIP2C_203	6578
1612	3398	5184	6970	784CIP2C_204	6662
1613	3399	5185	6971	784CIP2C_205	6672
1614	3400	5186	6972	784CIP2C_206	6691
1615	3401	5187	6973	784CIP2C_207	6695
1616	3402	5188	6974	784CIP2C_208	6746
1617	3403	5189	6975	784CIP2C_209	6898
1618	3404	5190	6976	784CIP2C_210	6938
1619	3405	5191	6977	784CIP2C_211	6943
1620	3406	5192	6978	784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C_213	7200
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7218
1624	3410	5196	6982	784CIP2C_216	7249
1625	3411	5197	6983	784CIP2C_217	7500
1626	3412	5198	6984	784CIP2C_218	7509
1627	3413	5199	6985	784CIP2C_219	7523
1628	3414	5200	6986	784CIP2C_220	7544
1629	3415	5201	6987	784CIP2C_221	7564
1630	3416	5202	6988	784CIP2C_222	7568
1631	3417	5203	6989	784CIP2C_223	7631
1632	3418	5204	6990	784CIP2C_224	7813
1633	3419	5205	6991	784CIP2C_225	7831
1634	3420	5206	6992	784CIP2C_226	7843
1635	3421	5207	6993	784CIP2C_227	7907
1636	3422	5208	6994	784CIP2C_228	7943
1637	3423	5209	6995	784CIP2C_229	8175
1638	3424	5210	6996	784CIP2C_230	8216
1639	3425	5211	6997	784CIP2C_231	8225
1640	3426	5212	6998	784CIP2C_232	8271
1641	3427	5213	6999	784CIP2C_233	8397
1642	3428	5214	7000	784CIP2C_234	8466
1643	3429	5215	7001	784CIP2C_235	8503
1644	3430	5216	7002	784CIP2C_236	8953
1645	3431	5217	7003	784CIP2C_237	9106
1646	3432	5218	7004	784CIP2C_238	9139
1647	3433	5219	7005	784CIP2C_239	9555
1648	3434	5220	7006	784CIP2C_240	9650
1649	3435	5221	7007	784CIP2C_241	9889
1650	3436	5222	7008	784CIP2C_242	9933
1651	3437	5223	7009	784CIP2C_243	9953
1652	3438	5224	7010	784CIP2C_244	9981
1653	3439	5225	7011	784CIP2D_1	746
1654	3440	5226	7012	784CIP2D_2	3558
1655	3441	5227	7013	784CIP2D_3	3558
1656	3442	5228	7014	784CIP2D_4	3633
1657	3443	5229	7015	784CIP2D_5	3658
1658	3444	5230	7016	784CIP2D_6	3732
1659	3445	5231	7017	784CIP2D_7	4004
1660	3446	5232	7018	784CIP2D_8	4700
1661	3447	5233	7019	784CIP2D_9	4703
1662	3448	5234	7020	784CIP2D_10	4774
1663	3449	5235	7021	784CIP2D_11	4894
1664	3450	5236	7022	784CIP2D_12	4918
1665	3451	5237	7023	784CIP2D_13	5159
1666	3452	5238	7024	784CIP2D_14	7443
1667	3453	5239	7025	784CIP2D_15	8673
1668	3454	5240	7026	784CIP2D_16	8679
1669	3455	5241	7027	784CIP2D_17	8727
1670	3456	5242	7028	784CIP2D_18	8734
1671	3457	5243	7029	784CIP2D_19	8756

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1672	3458	5244	7030	784CIP2D_20	8818
1673	3459	5245	7031	784CIP2D_21	8844
1674	3460	5246	7032	784CIP2D_22	8846
1675	3461	5247	7033	784CIP2D_23	8912
1676	3462	5248	7034	784CIP2D_24	8918
1677	3463	5249	7035	784CIP2D_25	8918
1678	3464	5250	7036	784CIP2D_26	8941
1679	3465	5251	7037	784CIP2D_27	8941
1680	3466	5252	7038	784CIP2D_28	8951
1681	3467	5253	7039	784CIP2D_29	8951
1682	3468	5254	7040	784CIP2D_30	9007
1683	3469	5255	7041	784CIP2D_31	9012
1684	3470	5256	7042	784CIP2D_32	9013
1685	3471	5257	7043	784CIP2D_33	9025
1686	3472	5258	7044	784CIP2D_34	9051
1687	3473	5259	7045	784CIP2D_35	9054
1688	3474	5260	7046	784CIP2D_36	9054
1689	3475	5261	7047	784CIP2D_37	9113
1690	3476	5262	7048	784CIP2D_38	9134
1691	3477	5263	7049	784CIP2D_39	9152
1692	3478	5264	7050	784CIP2D_40	9152
1693	3479	5265	7051	784CIP2D_41	9211
1694	3480	5266	7052	784CIP2D_42	9223
1695	3481	5267	7053	784CIP2D_43	9223
1696	3482	5268	7054	784CIP2D_44	9231
1697	3483	5269	7055	784CIP2D_45	9236
1698	3484	5270	7056	784CIP2D_46	9236
1699	3485	5271	7057	784CIP2D_47	9303
1700	3486	5272	7058	784CIP2D_48	9309
1701	3487	5273	7059	784CIP2D_49	9314
1702	3488	5274	7060	784CIP2D_50	9326
1703	3489	5275	7061	784CIP2D_51	9339
1704	3490	5276	7062	784CIP2D_52	9348
1705	3491	5277	7063	784CIP2D_53	9376
1706	3492	5278	7064	784CIP2D_54	9382
1707	3493	5279	7065	784CIP2D_55	9407
1708	3494	5280	7066	784CIP2D_56	9414
1709	3495	5281	7067	784CIP2D_57	9439
1710	3496	5282	7068	784CIP2D_58	9485
1711	3497	5283	7069	784CIP2D_59	9493
1712	3498	5284	7070	784CIP2D_60	9501
1713	3499	5285	7071	784CIP2D_61	9526
1714	3500	5286	7072	784CIP2D_62	9526
1715	3501	5287	7073	784CIP2D_63	9551
1716	3502	5288	7074	784CIP2D_64	9557
1717	3503	5289	7075	784CIP2D_65	9568
1718	3504	5290	7076	784CIP2D_66	9588
1719	3505	5291	7077	784CIP2D_67	9597
1720	3506	5292	7078	784CIP2D_68	9615
1721	3507	5293	7079	784CIP2D_69	9628
1722	3508	5294	7080	784CIP2D_70	9649
1723	3509	5295	7081	784CIP2D_71	9652
1724	3510	5296	7082	784CIP2D_72	9660
1725	3511	5297	7083	784CIP2D_73	9662
1726	3512	5298	7084	784CIP2D_74	9725
1727	3513	5299	7085	784CIP2D_75	9746
1728	3514	5300	7086	784CIP2D_76	9777
1729	3515	5301	7087	784CIP2D_77	9787
1730	3516	5302	7088	784CIP2D_78	9790
1731	3517	5303	7089	784CIP2D_79	9842
1732	3518	5304	7090	784CIP2D_80	9842
1733	3519	5305	7091	784CIP2D_81	9848

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO:in U.S.S.N. 09/488,725
1734	3520	5306	7092	784CIP2D_82	9867
1735	3521	5307	7093	784CIP2D_83	10010
1736	3522	5308	7094	784CIP2D_84	10011
1737	3523	5309	7095	784CIP2D_85	10052
1738	3524	5310	7096	784CIP2D_86	10057
1739	3525	5311	7097	784CIP2D_87	10085
1740	3526	5312	7098	784CIP2D_89	10139
1741	3527	5313	7099	784CIP2D_90	10142
1742	3528	5314	7100	784CIP2D_92	10165
1743	3529	5315	7101	784CIP2D_93	10173
1744	3530	5316	7102	784CIP2D_94	10173
1745	3531	5317	7103	784CIP2D_95	10273
1746	3532	5318	7104	784CIP2E_1	3121
1747	3533	5319	7105	784CIP2E_2	3628
1748	3534	5320	7106	784CIP2E_4	3673
1749	3535	5321	7107	784CIP2E_5	4018
1750	3536	5322	7108	784CIP2E_6	4467
1751	3537	5323	7109	784CIP2E_7	4865
1752	3538	5324	7110	784CIP2E_8	4916
1753	3539	5325	7111	784CIP2E_9	4923
1754	3540	5326	7112	784CIP2E_10	4926
1755	3541	5327	7113	784CIP2E_11	4962
1756	3542	5328	7114	784CIP2E_12	4963
1757	3543	5329	7115	784CIP2E_13	4964
1758	3544	5330	7116	784CIP2E_14	4988
1759	3545	5331	7117	784CIP2E_15	5835
1760	3546	5332	7118	784CIP2E_16	7682
1761	3547	5333	7119	784CIP2E_17	7682
1762	3548	5334	7120	784CIP2E_18	7699
1763	3549	5335	7121	784CIP2E_19	7707
1764	3550	5336	7122	784CIP2E_20	7707
1765	3551	5337	7123	784CIP2E_21	7752
1766	3552	5338	7124	784CIP2E_22	8357
1767	3553	5339	7125	784CIP2E_23	9065
1768	3554	5340	7126	784CIP2E_24	9324
1769	3555	5341	7127	784CIP2F_1	2976
1770	3556	5342	7128	784CIP2F_2	3559
1771	3557	5343	7129	784CIP2F_3	4021
1772	3558	5344	7130	784CIP2F_4	4474
1773	3559	5345	7131	784CIP2F_5	4566
1774	3560	5346	7132	784CIP2F_6	4705
1775	3561	5347	7133	784CIP2F_7	4707
1776	3562	5348	7134	784CIP2F_8	4712
1777	3563	5349	7135	784CIP2F_9	5008
1778	3564	5350	7136	784CIP2F_10	5009
1779	3565	5351	7137	784CIP2F_11	5015
1780	3566	5352	7138	784CIP2F_12	5015
1781	3567	5353	7139	784CIP2F_13	7724
1782	3568	5354	7140	784CIP2F_14	7725
1783	3569	5355	7141	784CIP2F_15	8828
1784	3570	5356	7142	784CIP2F_16	8830
1785	3571	5357	7143	784CIP2F_17	9739
1786	3572	5358	7144	784CIP2F_18	9896

TRADOCS:1416247.1(%CS7011.DOC)

TABLE 7

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine; M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKILLAWSPVIAPG ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL VLALFAFVGPMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW KITQF
5360	2	1115	PRVRSSGGQBDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF VVLPTGDVWSRPDGSYLNKLLITRARQDDAGNYICLGANTMGYS FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS SSKHLWYMPEEYIRQGKLSIKTDVYSFGIVIWEVLTGCRVVLDD PKHIQLRDLLRELMEKRGLDSCLSPLDKKVPPCPRNFSAKLPCL AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSPRC PSFLPLENVPSIPVEDDESQNVNLLPSDEGLRIDRMTQKTPPEC SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWPPKYIVPSQD LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKPSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQKA NNLNTPNNGKFVYFLPSPVNSSNPPFTSQTKANGNPACSAQLQH VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ MENLPSTALPAQMEDLTKTVLPLNIDRGSDPPLSLPARSSSIDL FPSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK RAKWPAIIRDGKPICSRCYRAPTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVPPTNDLLLKTVEN GLCSSSPPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS ASKRRKKVAPPLIAPNASQNLVTSDLTTWQLIAKSVEIPTTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLPMTDVKSNFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQSILEGL QXLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYQRKSQSENVPASRSTQVKKQLAMTEENKKESQ PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSSLQVITVTS EQCNTNALTNTQTKGRKIRRHKKEKSEKKRKKPVSQSLEFPTRY SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI KMPKTKRKKXNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKESEQEGAKNDVKDSDTCVSESND NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE KAEPASAAELSSVRKEESTAVAIQTIEEHPASFDWSSFKPMGPE VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV TSGNHVCPCKESETPVQPANPSQLQCSDNVKIVLDKNLKDCTEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, K=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDYSIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPPPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNT?\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPPPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTVSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGPRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5365	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPPPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHPFFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVPI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQ3GEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKKNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGPKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5366	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRHEANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK PEAEETCFDKYTGNTYRVGDTYERPKDSNIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KYSFCTDHTVLVQTRGGNSNGALCHPFFLYNNHNYTDCTSEGRR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST PVTSNT\VTGETTPPSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV KVTIMNTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVGKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKKNQKSEPLIGRKKTDELP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGPKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5367	235	3591	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIYHVLRL ILELWMTRLLLEKSVSLQTQYLLLIVKILGWPPGKEMRHHLQIM EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKELV KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM SILRSQCQISLDVTLSVPNVSEGIVRLLLDPQTNTEIANYPIYKI LFCVRGHDGTPESDCFAPTESHYNAELFRIHVFRCEIQEAVSRI LYSFATAFRRSAKQTPLSATAAPQTPDSDIPTFSVSLEIKEDDG KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNKELAIERCF GLLLSPGKDVRNSDNHLLDLESMGKSSDQKSYVITGSNNPKSPH PQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLES ESEEERRKTTASPSVRLPQSGSQSSSVIPSPPEDDEEEDNDEPLL SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKQLSSLVRNGV PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQDSAITRDIN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RTFPAHDYFKDTGGDGQDSLYKICKAVSVYDEEIGYCQGQSPLA AVLLLHMPEEQAFSVLVKIMPDYGLRELFKQNFEDLHCKFYQLE RLMQEYIPDLYNHFLDISLEAHMYASQNFLTLFTAKFPLYMVFH IIDLLLCEGISVIFNVALGLLKTSKDDLLITDFEGALKFYRVQL PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD NAEEKADALNKELLMTKQKLIDAEEEKRRLEEESAHLKKMCRRE LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL REMELELAQTKL\QLVEAECKIQD\LEHPF*GLPFNE\VQAA\K KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTWLDPAIFAVTPLLALVGAVLYLYPAS RQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW WWQCS*KP\QRKKLYENGVTDSLKSNFALLLKLPEELDKWLSY PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG TVWSEIGKGFLDGSLDKNWTRKKQYEDALMQLESVLRNIIKERK GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW AIWFLTTSEEVQKKLYERINQVFGNGPVTPEKIEQLRYCQHVLC ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY.
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED CHCNLFCLADLTGIKWKKYVWQQPTSAPILFPVTEEDPILSSFS RCLKADVLG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLFTMTY QKKKMECGRMDFPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF VKPYEKDEKPINKSEHLSCSFTPFLHGDSNVCTSVEINQHQPVY LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLTPPTSPEEVQTVDPQSVQKNVKFSSVSDGFNSDSTSHH GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEEATA AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMPAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKPGNNSGLFFEDELD IIGRNTDCGKEAEKRPEALRATSAEHVNGGLRESEKLSDDLILL LQDQCTNLFSPFGAADQDPPPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYFSCRLGQHRPVSRLL TDGINRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH AVIYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQVLLQPVKHEDREIYPQHLKSLAVSAP TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRNILASC TDLYGELLETCIINIDVPNRARRKKSSARRPGLQKLWRWCLGLV QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM CRMCGISAADSPSILSACLVAMEPQQSFVIMPDSVSTGSVFGRS TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL APNPNNDGADGMGIFDLLDTGDDLDPDIINILPA3PTG3PVH3P GSHYPHGGDAGKGQSTDRLLSTBPHEEVPNILQQPLALGYFVST AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH PVVLNQLYNFIMNML
5370	1226	716	RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPPLACFTYTTDKQS SKENTRTVEKLYKCSVDIRKIRR*KDGYP*RMKPMLKKLRI/P LQELGADETAVASILERCPEAIVCSPTAVNTQRKLMQLVCKNEE ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSQ NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG HLANLNGSKKEPEANPGKIQAKKVRPLFNPVAPLNVBE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME PLRLLILLFVTELSGAHNTTVFQQVAGQSLQVSCPYDSMKHWGR RKAWCRQLGEKGPCQRVVSTHNLMLLSFLRRWNGSTAITDDTLG GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD HRDAGDLWPPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSPS SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS KLCQG
5373	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVPNYSPPRTPYTPNSQV QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDPSGKAKPS PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTN\TEI YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ \QEADAE\VNTETLNKSSQGSSSSTQSASPSETASA\SKEKETSA EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPPLGTSK
5374	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVPNYSPPRTPYTPNSQV QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TNPVEIKERLKSTSPASEKADPGAVKDKASDEPEKDPSQKAKPS PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC ANFKKEAIPYCCWNTSYCDYPCQ\QAHWPBH\MKSCTQSATAPQ \QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5375	2907	1116	HIFLAEEEPNLERRCRGPLAMGPAQPRLLSGPSQESPQTLGKES RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR RCQA/RGLPLPCPECGRRFRHAPPLALHRQVHAAATPDWGPACH LCGQSFRGWVALVLHLRAHSAAKAGPPACPKMARDAFWRRKAAS SSILRRCHPSRPRGPRPPICGNCGRSILPTWDQ/LKVAHKRVHV SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\QCA CCGKRFRHK\PNLIRSHAACTSGERPHO/CSRECG\KRFTNKPY LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP QDPIEAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPFTCAEC GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN SAEPNAPRFGPFVCPDCGKAFRHKPYLAAHRPIATPAEKPYVCP DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP VLTSPGAVPPLPSPSKBSEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEEKGSDGRASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETPDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGCEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGESLSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSE-PAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS
5377	762	1106	DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP
5378	2009	664	QASGTTLRPLPDLPQLKRRRATSRNRALKPRGRLVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SFSFRNSKQTYSGVPIIAANNDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV BELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG BLIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PPKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTPIRVTQQ VNPIFSEAC
5379	2009	664	QASGTTLRPLPDLPQLKRRRATSRNRALKPRGRLVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR SFSFRNSKQTYSGVPIIAANNDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV BELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG BLIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PPKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTPIRVTQQ VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRRSERSLSAPGNLLTKKPTRECESL SRLKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPPLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLMWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM
5381	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPPLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLMWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM
5382	1536	203	GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAQAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANPIQYLLDPHTEKLAPFNEH WRQVYRLCHPCQIDYDPVGKLETLDEDAAQLLQLLQVDLAAPLP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADPVLFGYPKP ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISPGMYSABELKKLS VKSITNPRYLDSLGNPSANGLYDLALGFADSKEVCSTCVQDFSN CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC PHCKTGRSVVRKRHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN PSVFFLDFLVVPPSRSRPVSRLGDQMPTNGQTVNLQAVMKDVVL IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSFLSTLPGQ SLIDKLYNIWIRLQSIVNIVFDSEMDKLMMDKYPGIRQILEKKE GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVPATKLTYP QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH RPSIQAHKARILPEEKVLRLHYANCKAYNADFDGDEMNAHFPQS ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG CPFTREHYMELVYRGLTDKVGRVKLLSPSILKPPPLWTGKQVVS TLLINIIPEDHIPINLSGKAKITGKAWVKETPRSVPGFNPDSMC ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIEESTH CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG RPLTGIKPPEFFFHCMAGREGLVDTAVKTSRSGVLQRCIIKHLE GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPPLA SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR RGAPLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESPCMEEKQNKFQVYQLRFQPLPHAYYQQEKCLRPEDILRFMET RFFKLLMESIKKKNNKASAFRVVNTRRATQRDLDNAGELGRSRG EQEGDEEEEGHIVDAEABEGDADASDAKRKEKQSEEVDYESEEE EEREGEENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCP EGVYKPLNRPGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLPELKQPLR
5384	196	886	QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVPVNLDGCFDMAT GQFAAPLRGIYFPSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITP SGHLIKAEDD
5385	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT
5386	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVPTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT
5387	2	2117	FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLPGRRWAIA SDDLVFPGFFSLVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIAA TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLRTAAT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SVWETRIKLLCCCYGKDDHTRVAPSSTAELFSTVFSDTDLVPSD IAAGLALLHQQQDNIRNNQEPAQVVCHAPQSSQEADLDAELKNC HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M VGGDQLQL/CTSAPILHTHRAAVQGLHIPRQLPWTRFTELPFLVA LDHRKESVVVAVRGTMSLQDVLTDLSAESSVLDVECEVQDRLAH KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA ALLATWVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLIHGLMYELPG GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL DSSPKYPPLYPPGRIIHLQEEGASGRPGCCSAAHYSAKWSHEAE FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAQQVSSV DVA
5388	1569	753	TADGGAGGGGRRQAGVRRHYLYPPTGGVRRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPNLCSTGCGPYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN
5389	1569	753	TADGGAGGGGRRQAGVRRHYLYPPTGGVRRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGPYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN
5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAPKRIRLRPRYLRDVSEVDTRTTIQGEEI SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTPASCS LEDIVIAAPEGLRWPQLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEPHTSMA\ LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQEQLKVMPVGGPNTRKDYHIEEGEEVFYQLEGDM VLRVLEQQKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS SEQYRTGKPIPDQLLKEPPFFLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLPGDTYETQVIAYGQGSSBGLRQNVDVWLMQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
5392	1	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDNTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNVYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PPEDALKLHECSVAAGVTAAPLPLRDQMPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAARRMLRADGDPLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP PKAVLKLEPPNINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			\WLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV LSEWLVLQTPHLEPQEGETIMLRCHS\WRDKP\LVKVTFFQNGK SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP RAPTDDDKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP PKAVLXLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG \NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV LSEWLVLQTPHLEPQEGETIMLRCHS\WRDKP\LVKVTFFQNGK SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL PQQSYNFDPDTCDESVDPPKTSSKTPSSPSKSPASFEIPASAME ANGVDGDGLNKPAKKKKTPLKTDTPRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5396	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL PQQSYNFDPDTCDESVDPPKTSSKTPSSPSKSPASFEIPASAME ANGVDGDGLNKPAKKKTPLKTDTPRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asperagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PQQSYNFDPDTCDESVDPPKTSSKTPSSPSKSPASFEIPASAME ANGVDGDGLNKPAKKKTPLKTDTPRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNFNQEGVPRFSYVFSADFIARPSEINFDGIKLDLS HEPSLVAPNTEANSFESKDYLQVCLRIRPPTQSEKELESEGCVH ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFPPGFLGPAT TQKEFFQGCIMHP\VKDLLKGQSRLIPTYGLTNSGKTYTFQGTB ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSREYLRLSSEQEK EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKRK MLRLSQDVKGYSPIKDLQWIQVSDSKEAYRLLKLGIKHQSVAFT KLNNASSRS:HSIPTVKILQIEDSEMSRVIRVSELSLCDLAGSER TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQQHVP FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK TLEENKAPISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG KCDTREEAAKDICATKVETEEATACLELKFNQIKAELAKTKGEL IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDQ KEDTINEPQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK SEEVRPNIABIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE LNKQIVHPQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK SKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL DSVSQISNIDLLNLRDLSNGSEEDNLPNTQLDLLGNDYLVSKQV KEYRIQEPNRENSPHSSIEAIWEECKEIVKASSKKSHQIEELEQ QIEKLQAEVKGYKDENNRLKEKEHKNQDDLLKEKETLIQQLKEE LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK LKEELSASSARTQN\LNADLQRKEEDYADLKEKLTDAKKQIKQV QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK EQLINQKVEEAIQQYERACKDLNVKEKIIEDMRMTLEEQEQTQV EQDQVL\EAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKEA ENIRNKEMKKYAEDRERFFKQQNEMEILTAQLTEKDSDLQKWRE ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKPGDFLQHS PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK
5399	705	230	GPRMAXFLSQDQINEYKECFSLVDKQQRGKIKATDLMVAMKCLG ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE ILLAMLMVDKSKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE \ADIEPNGKVKYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIDPTNYPASRAALVAQNYINVQQGTPHRVFEVQKVK QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE TAPEVNFTFEGETGKNPDEEDNTFYQRLKSMKEPLEAQNI\PDN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIQTVKQV QRNDDPIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS RLPKEVQLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPPKLLIHPQAVVRLSCGAGSMGS QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVPWTWMFSTYFME KWAPRQDDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\ VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY DNRVSVAARHAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA FPGPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLPRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
5404	187	1111	LPVTLYFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIYYDYGT DNFEESIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY LYARFNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL SLVEELSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYERETQPTA ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIPYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLESCPSRGQGKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEPCLEEWQCLDTAQQNLYRNVMLENY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RNLVPLG/IIAVSKPDLIYTCLEQEKEPWEPNRRHEMVAKPPVMC SHFTQDFWPEQHIKDPPQKATLRRYKNCEHKNVHLKKDHKSVDE CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS HTEKKLPKCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAP NCPSIITKHKRINTGEKPYTCEECGKVFNWSSRLTTHKKNYTRY KLYKCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNQSS NLTEHKKIHPGEKPYKCEECGKAFNWPSTLTKHKRIHTGEKPYT CEECGKAFNQFSNLTTHKRIHTA\EKPYKCTECGEAFSRS\SNL TKHKEIHTEKKPYKCEECGKAFKWSSKLTEHKLTHTGEKPYKCE KCGKAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK AFKWSSKLTEHKITHTGEKPYKCEECGKAFNHFSILTKHKRIHT GEKPYKCEECGKAFTQSSNLTTHKKIHTGEKFYKCEECGKAFTQ SSNLTTHKKIHTGGKPYKCEECGKAFNQFSTLTKHKIIHTEEKP YKCEECGKAFKWSSTLTKHKIIHTGEKPYKCEECG\KAPKLSST LSTHKIIHTGEKPYKCEKCGKAPNRPSNLIEHKKIHTGEQPYKC EECGKAFNYSSHLNTHKRIHTKEQPYKCKECGKAFNQYSNLTTH NKIHTGEKLYKPEDVTVILTTPQTFSNIK
5407	3	659	RPRRRQSSCCTGNLAGWLLRAAPRFCRRTETDNEQGKGLAVLTL AIILLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWF KDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFIAQTGMEFR QS\RASDRQTLLP\NDPAPTQPLKDPRKMTQVSHLQQN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK NFTNGNVNGHMPSLPDSPPTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVMIQVGRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAPLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSQTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAQQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHSACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQPLPK TDGKKMADTSSMDSDFESDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TQTDFSSSPSTNEMPTLTTNGDLPRPIFIPNGMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPPTGYIIAVHRKMMRTELYFLSSQKNR PSLPGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAPLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKG PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGPLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRFPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRV VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSPGKPSPVTGLRAARRRRTRPSAPAAPSVGC GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQPN GGEPFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QQISNFFHKEANFWPEVSGYLISPLRSPFVDPALEWSLMASPWN KMEGESSRPEIHTPVSDKKKKXCSIHKERPQKHSHEIFRDSSLV NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK KRRYSALEVDEEAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA HKNKSKKKKKRSSNREYET\LAMPEGSQAGREAGTDMQESQPTV GLDDETPQLLGPTHKKKSKKKKKKSNHQEFESLAMPEGSQVGS EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKSNHQEF EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY LSADSGDADDSDADLGSAVKQLQEPIPNIKDRATSTIKRMYRDD LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDNKTIGEMVARRSL SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQELK EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS KWTSILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNEI DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYL YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVPPFRDIFYYEDD SEGGGHRKRKRRPRRHAWPTPVIPVLWRAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP HPPPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSQIPQ IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH SGSVIAAGISQGRSTSLKRDPKIFEYLRRDTEKRDPVSAGAAAG VSAAFGAPVGGVLFSLEEGASFWNQPLTWRIFFASMISTFTLNF VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SVVSLFHDPPGSYNPLTLGLPTLVYFFLACWTVGLTVSAGVPIP SLLIGAAWGRLFGISLSLYLTGAAIWADPGKYALMGAAAAQLGGIV RMTLSLTVINMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV DVLSDTASNHNGFPVVVEHADDTQPARLQGLILRSQLIVLLKHKV FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD LSEFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG LVTRKDLARYRLGKRGLEELSLAQT
5414	2130	390	GVASAWDRALPSPLLSPTSRVPRTSPPRCVSTETGRRDHARVPS QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCQGPRGTRSP RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINLLNYMDRPTV AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY STIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKD MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL NPTSWWADLRALARNPSFVLSSLGFTAVAPVTGSLALWAPAFLL RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYTF IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD AGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGG AAFLGTAHLH
5415	693	2986	IPFKTKLELQKH\LTTLT\NQEQATIPEEVQKLRPRNEQRENEL IISFLRCLFEEKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF RLDMLKNKAKRSLTESLESILSRGNKARGLQEHSISVDLDSSLS STLSNTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPE EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPPGPPPE EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ GVP\RHHRGEIWKFLAEQFHLKHQPPSKQQPKDVPYKELLKQLT SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGYCQGLSFVAGILLLHMSEEEAFKNLKPLMFDMGLRKQYRPDM IILQIQMYQLSRLLHDYHRDLYNHLEEHEIGPSLYAAPWFLTMP ASQFPLGFVARVFDMIFLQGTEVIPKVALSLLGSHKPLILQHEN LETIVDPIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD
5416	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPPLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF RRPRLASFGGMGTTSSLPSPVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPNHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIK3FRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAPQEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD ESSSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELPGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5417	27	4074	KSQLPCPWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGINTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF RRPRLASPGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVPSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVGVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD ESSSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELPGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5418	24	1133	SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLPGPLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVPKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQRAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF
5419	1395	259	GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAPGRRKSEEEGERRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCNMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIPCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECIISTLLPATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/ LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPRGMQGTSLGQVSFSKLGSPGAVIQVVLIFYLMVSSVVGP YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL TRFDLLGDPGRPNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV RAELIRAFGERE
5421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/ LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPRGMQGTSLGQVSFSKLGSPGAVIQVVLIFYLMVSSVVGP YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL TRFDLLGDPGRPNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV RAELIRAFGERE
5422	3	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF KAQCNWWHLSRDQAQVQRCDLGSSQPPPLGPKRFSCLSLPSSWD YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR TVPVSERELDWAKVMVEKSRMGVVPPGTQVEQLLYAKKLYDSAF HPDTGEKMNVIGRMSPQLPGGMIITGPMLQFYRTMPAVIFWQMV NQSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH FMCKVKVL/SAPLQVMLSGICFLIPMVPVACGLFPQKCELPVSYL EPKLQDTIKAKYGELEPVVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERRLDIPGPMSGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQQHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL GRRRLSPQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDSY LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG EGSLGSSQALGVSSGLLKTRPSLPARLDRNPFSDPDVEGQLPRK GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQQHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SQLASTPRAPQSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSPRPERERKRTSQSARRPTCTESRWKSEEVESDDEY LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGRILLQCLLE NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV
5425	1086	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK NCSWEVAYLPSEAGSLIP
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL	
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQ?AGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDBKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVBLGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5428	3	1839	SSRSERLSACAYAPPWLVSSRPARPAQLQRPQKMVEDGAEELED LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKPSAHRIV LAASIPYPHAMFTNDMMECKQDEIVMQGMDPSALEALINFAYNG NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV RQFAETMMCAVLYDAANSFIHQHFVEVSMSEEFLALPLEDVLEL VSRDELNVKSEEQVFEAALAWVRYDREQRGTPL\RNLQSNIRLL FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT TGQSNL\SSVGDVLTPRTDCWTFM\APMACHEGGVGVGCIPLLT I
5429	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF AQRERPHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQ LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNS GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSPQHQQSSGPPSL LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL
5430	441	1507	QKRKRRRRKKIMKTIQPKMHNSISWAIPTGLAALCLPQGVPVRS GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP TVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDV\A APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYQNYT CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL HLLLKF
5431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPFAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLVDRPHMAHGYEAPPPFAPRSPAWRARSKPV\ LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5433	360	1885	SVQEDKVGPEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV LPGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF SLIFTLGSFMNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			IAFTSAGSAVLLFLAMPMLTIGGILPLITNLQIGNLFGQHRSTI ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREQ/QQLSMKT GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRPAWHLVWL SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAPTQFGVL CAPWNGLLMDRLKQKYQKEARRTGSSTLAVALCSTVPSLALTSL LCLGPALCASVPILPLQYLTFILQVISRSFLYGSNAAPLTLAFP SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF MLAILLTFFHPFLVYRECRTWKESPSAIA
5434	66	652	RYAALYISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV LRQGRFGMFIGCINYPECEHTRLIDKPDETAITCPQCRTGHLVQ RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSQRLAEWSNAKERKHAKKMRNQPTNVTLSSGPVADRGVKH HSGGEKPPQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV TQKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWIAK RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEWN RPRLIGPLSHSILTEAIKAASVHTVGEDTERTPHRNWIETCKKP DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV TGEDRLGWGSGNDVLLPKGWGMAFWFPFIYRGVRVGGLKESAVH SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE PHTMICVPAKEDPLQLHEDWHYCGPQESKHSDPFRSKILKQKEK KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ RGLVLLRPPASLQYRFARIAIEV
5436	1781	635	ASDSIPWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR RAEELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSARERALRG ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA GSSVLRELHTADSVVNGSAQADVPKELERERSGAAESPALVTPD SEKSAKHGSGAPYSPELLSALTLRFEAPDSRNRWDRPLFTLVGL EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSPLHQLDQVTS QVLAQLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMPLRRLGGWLPRPWGRKKPMRPDPPVPE PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRRKELLGWLR GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR AALDTLGLRGPLGLWLHGLLSPLAALHGLHAVLSLLTAHPLHPA CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG KGL
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK NCEVEQVKGVTYSLESPLGPRMCTEDLPFPPAASCDSFKNQLVT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE DLHHYRNLSEPFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5440	693	253	EPIPVTPDHRLVTMTHIV\QTPSPVNS\GQPPNYEMLKEEQEVA MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAPFSFIN NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP ALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE LVQPPSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQNLQLVLL PPALFIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW SEPFSPGEGEQSLTNAIWVNEETKLVYPQGTKDTPLEHHLYVVS YEAAGEIVRLTTPGPSHSCSMSQNFTMFVSHYSSVSTPPCVHVY KLSGPDDDDPLHKQPRFWASMMERAAKIFHFHTRSDVRLYGMIYKP HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKEAPAE APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG KELPDKPTIKWFKGKWLELGSKSGARPSPKESHNSASNVYTVEL HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQDASGQSL ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK KSAAFTKKLDPAYQVDRGNKIKLMVEISDPDLTLKWPKNGQEIK PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCPTELFV KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEEGAQVMWMKDGVEL TREDSPKARYRPKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYK NGVEVRPSKRITISHVGRPHKLVIDDVRPEDEGDYTPVPDGYAL GSLSAKLNFLEIKVEYVPKQ\EPPKIPLGFASGGKTSENAD/IV VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVPTTTEGRTRIE KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIPLQVVDVP DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ RWMKLNFEVPTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIQAGGIDGY LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN IAGRSEPATLAQPVTIRSIAEPPKIRLPRHLRQTYIRKVGEQLN LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVPFVRQAA RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWPNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV NELGEALAECKLEVRVPQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSPRRSRSAAEPA MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPPITFNSEVKTDV NKIEEPLEEVLCPPKYLKLSPKHPESNTAGMDIPAKFSAYIKNS RPEANEALERGLLKTLQKLDSYLNSPLPDEIDENSMEDIKFSTR KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPFQPPTPDVTESDILRAY RAQKNLDFEDPY*DSESRLEPDPAGPGDSRNPGDAKYGSPKHRL IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHPAPPDDG YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR QSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPG SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q *PDWGDRRPNGQVATGLPELWGAEAPSAAAHPGLHRERHPEGLP RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSQAPAH QGGGCGYGQSQGPSGRPRGGAGSRH
5445	2364	486	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP EEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ DVLGIRQLERPLPLTSVCYPQDLPRPLRSRSFPQFEPQRYPACA QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP ALPGQ?LPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG LPRHQDQPHIQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ DVEGAESQLDRDEHGLHTKYIHRMMQIEFIKQGSMNFRPIPVLP PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEERYELKEGQ TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA RFKQVKLSRNFPKSSFHAQSESSTVGKNGSSFQKKKCEDCVVPY TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF IQPYLNSHYKETTVPRKVLPHLRGHRGPVNTIQWCPVLSKSHML LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG GFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD ASTRDSADRTIIANDFRTSAKISNQIFHERFTCPSLALHPREPV FLAQTNGNYLALPSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG GDLLVTGSADGRVLMYSPRTASRACTLQGHTQACVGTTYHPVLP SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFPPPFPF RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGVSL RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKDGTGCSGRCSSSR QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPNLHSSHPGLEKISAIVWEGNDCKKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFPPPFPF RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGVSL RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	8136	1242	GQQPASPFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA AGCRLEEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPGL PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRK SQVLPSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTPCVLGT SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN LSVETNAVGQDVSVLPRVTGALQFGELQKHSTGGVEGAEWWATQ AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGPS PPTFHYEVVQAPRKGNLQLQGTRLSDGOGFTQDDIQAGRVTYGA TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG TQDKTTMVTSPTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE SSGDMAWEEVRGVFRVAIQPVNDHAPVQTIGRIPHVARGGRRLL TTDDVAFSDADSGPADAQLVLTRKDLLFGSIVAVDEPTRPIYRF TQEDLRKRRVLPVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT AGPRNGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAQYLVMVSRQALADEPPS LDPVQSPSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYPPT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT TNTGLQMWEGATAPIPAEALRSTDGDSGSEDLVYTIEQPSNGRV VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGQLV YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN ERPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV IIPMCLVLLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP ALKNGQYWV
5451	1	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR KNSEPGSPHSLEALRDAAPSQGLNFLLLPTKMLFIFNFLFSPLP TPALICILTFGAAIFLWLITRPQPVLPLLDLWNQSVGIEGGARK GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW IISSLACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILFLLFGCLGVPGLFRLLQ WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT KALLPSMIKRRQGHIVAISSIQGKMSIPFNSAYAASKHATQAFF DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQQELKNLRACVLEL EERLSTQEGLVQELQKKQVELQEBRRGLMSQLEEKERRLQTSEA ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL QELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPQGDPQLEGLIPR ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG QGGECEIRRAGPQSEELTVTNARYVPVSCEKEVDALLHLARQNR AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF ASKVEPSVLFQTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP MSMYRVRGGRVAGGCPIGWRAPCPRAIK
5457	2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP TADRGDAAATDDPAARPQVQKHSWDGLRSIIHGSRKYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV RKEALLLLSWKQMLDHFQATPHHGVYSRSEELLRERKRLGVPGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW EGSEGLKTLRILYEEVDESHVEVIHVPSPALEERRTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS
5458	6642	4022	FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAPGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVRI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEPEQLKHEIKRLEEETPYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDQLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGHLREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ AAVDRTTELSRQRIASQELGPAVDKDKEALMEEILKLKSLLSTK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			REQITTLRTVLKANKQTAEVALANLKSKYENEKAMVTETMMKLR NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAARDE KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP DLLATGVEREQSERFNVYLMPSPNLGCYMGECALQITYEYICLW DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP GLGLAZMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSDGNKKS ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK CEKCHHFFVVLSEADSKKSIIKEPESAABAVKLAPQQKPPPPPK KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDISEKDRL LRHVEARDLIEPGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRPGAPEAAVMELPSGPGPERLPD SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPPDH NIVNLLTTCSTPLLNSPPSFVCWSRGPMEMNGRGELVESLKRPC ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPPSIQDVVQPLTL QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRNLRPVHRQLG EANEEFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP QSAQSSFPPSPQPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKPPSSGPV TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA RLSNGSPSAPSLTNSRGSVHTVSPLLQIGLTRESVTIEAQELSL SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC KDCKFNCHKRCASKVPRDCLGZVTFNGEPSSLGTDTDIPMDIDN NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI SPSTSNNIPLMRVVQSIKHTKRKSSTMVXEGWMVHYTSRDNLRK RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHRRTGRDVAIKVIDKM RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP WLQDYQTWLDLREPETRIGERYITHESDDARNEIHAYTHNLVYP KHFIMAPNPDDMEEDP
5463	237	1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ YVMQVSAKDGQLLSTVVRTLATQSPPNDRPMCRICHEGSSQEDL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHPRPAVERKPR PLVEWLRNPGPQHEKRTLPGDMVCFLPITPLATISGWLCLRGAV DHLHFSSRLEAVGLIALTVALFTIYLPWTLVSFRYHCRLYNEWR RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQVHKTFVEEVQTTL GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI LAFDVTDLESFEALDIWRGDVLAKIVFMEQSYPMVLLGNKIDLA DRKYQSILENHLTESIKLSPNQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIPGVKQQGPAAVEA VNVFHHLPYEGQVDIYNINDPLKETATIGFINNPGQIPKQLPKK PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG HSDGVVRFWRMEPLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ DEDSSDSEADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAPDRKDNAHPA EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI SSPVRVCQNCYNLQHERGSEDGPRNC
5466	3	992	HACAHASAHASGRLVRWWRKHRSVMGIQTSPVLLASLGVGLVTL LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRP RFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL LTYTGXGHPNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV QLACHPNLDKLGYSQKNRFTY
5467	2103	4	GEALRVGTRGCRRDLPDPQARIPYIQKKDLEEDESVTAAHLKSRG RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL YRDVMLENYSHLISLAGSSISKPDVITLLEQSKEPWMVVRKETS RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICNT HXPYECKECGKYFSCUSNLIQHQSIHTGEKPYKCKECGKAFQLH IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLP ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY LQLSQHQKTHTGEKPFECKECGKFFRRGSNLNQHRSIHTGKKPF ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SPLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA DTTHPLTKHRKIASSFRDSSLPDIPTLSCNLLKQASGKNLNLND ESQHGLLMQLLKLTHNCLNFDPIGTSTDESSDDLCTVQIPTSWR SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQPRKIYIGDQVO KSSKLYRRLSEVLGLNDETMVLSVPIGKIITNLKYWGRCEPITS KTLQLLNDLSIGYSSVRKLVKLSAVQPMLNNHTSEHPSFLQINN QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE AVAQMPSTNSFNEQEAKRTLVGLVRDLRGIAFAPNAKTSPMMLF EWIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PDVSSPNGILLFRETSKMITNYGNRILTLGEVPKDQVYALKLKG ISICFSMLKAALSGSYVNPGVFRLYGDDALDNALQTPIKLLLSI PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ BSDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG LILLWEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL TKNRDRFTQNLSAFRREVNDSMKNSTVGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGHMKVLQ EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK SAWCPVEISKTVLWPESISVVRCVELFEAPVECEEEEEVEEEKG SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD MGESCLLPPSGSTSAHMPNDEFPSAGPKEAPPWGKEQPLHLEPS PPASPTQSPDNLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELG PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG YKAPSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA PVPVPLFTPGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM RVS
5470	17	1418	TACRIRTSLNRGIAAVKRDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAPPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE
5471	1868	658	RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLEELEKQMTS FYDSLGKINEIITVLERREAQSSALPKQKHQELLACQENCKKTLT LIEKGSQSVQKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK TGDWKKHVETNGRLMKKFEESRAELEKVLRIAQEGLEERGDPEE LLRRHTEPFSQLDQRVLNAFLKACDELTDILPEQEQQGLQEAVR KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RLMPQEGSEKIIKEHRVFPSDKGFHHLCEKRLQLIEELCVKLPV RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS EPSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTKRG ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSPKALVTLLS EVEKMLSNPGDCVQYKEIVKNSLEELISGSKEVQEQAEKILDTE NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG HEELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKETVVR YLFQTGSSHERFLSFSSLESLSSELEQTKEPSKRTEESIAVQAEN LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYVIDK S
5474	2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAPVKSGWLLRQSTI LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAWKFT LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGRTLS LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPVAGLYGQQ PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLPWVP
5475	2	506	ARGWLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGYYRF VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR
5476	192	1457	SDSMSLLDCPCTSRTQVESLRPEKQSETSIHQYLVDEPTLSNSR PSTRASEVLCSTNVSHYELQVEIGRGPDNLTSVHLARHTPTGTL VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR AVYDFPPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIPPQSESRMKNSQ SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEP
5477	3	1044	RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEBIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPPILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPSEFRKAAQQQE EQEEKBEEDDEQTLHRARENDDWKDTHPRGYGNRQNMG
5478	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGPVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHVQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5479	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGPVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHVQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5480	444	1952	LSLTSRMEEABLVKGRLQAITDKRKIQEEISQKRLKYEEDKLKH QHLKKKALREKWLLDQISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKABLQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDD3QNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQRRIKIKTNGLGIGVNESI HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMTPWEESNVWQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE DEEDVRYNIVHSLPPDINDTEPVTMIPMGYQQAEDSEEDKKFLT GYDGIIHAELVVIDDEEEEDEGSAEKPSYHPIAPHSQVYQPAKP TPLPRKRSEASPHEKHKS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLPLLLHESPQPPALRV VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVPSSQQQSELILL QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAIV AKGKSVFLDQMKKFVEWLQNAEEESESEGEEN
5482	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGP GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP VMVPAQSQAGSLV
5483	1	788	FPFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA ENRIKQLETDSSEEISRYQEMIQKLQNVLSSERENCGLVSEQRL KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG FEVQLREMEDSNRNSIVELRHLLATQQKANRWKEETKKLTESA EIRINNLKSELSRQKLHTQELLSQLEMANEKVAENEKLILEHQE KANRLQRRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDQENAASGSNASGS ESDQDSRGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEKANSDDERPVA SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE DEPEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD PECQRTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ AQTN
5485	161	1074	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPEFATSGVAA VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN DFICGGLLGAMLGPLFFPINVVKTRIQSQIGGSFQSFPKVFQKI WLERDRKLINLFRGAHLNYHRSLISWGIINATYEFLLKVI
5486	1404	142	IPGSTISNSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR PAAGKEAQKGPLLPDDLPPASSTDSGSGGPLLFDDLPPASSGDS GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY PAVFDGHGGIRASKPAAQNLHQNLIRKFPKGDVISVEKTVKRCL LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPADVPLPLQPCPSNCDMERVTLALLLLAGLTA LEANDPFANKDDPPYYDNKNLQLSGLICGGLLAIAGIAAVLSGK CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH GHKFFIGFGGKGANQCVQAARLQAMTSMVCKVGKDSFGNDYIEN LKQNDISTEFTYQTKDAATGTASIIVNNEQGNIIVIVAGANLLL NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD TTVSPKI
5489	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKNPLLLLGETEPLK LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSP FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP GEDEDS
5490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKNPLLLLGETEPLK LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSP FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPVTQSKEDRPDTEGRSE QGDMASSFLPAGAITGDSGGELSSGDDSGEVEPPHSPEIEETSC LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP SFFDFEGKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI PEKKGKSANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQHRAD INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP EEVTGCKTVSLVLQRHTTGKA
5492	3	1896	ASKNPLSAVCTTGIMSSLAVRDDPAMDRSLRSVPVGNIPYEATEE QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP IDPEDAPESITRAVASLPPEQMFELMKQMKLCVQNSHQEARNML LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ SVSVSGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRPVKDI PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGNPG VGPVPLERGGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHENRG GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMSTE VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGGAGIQGGAGSQGGSQ PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDPVRTLA EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDNKTTNLE EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQQYVEW SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL QAKADLEKELECAREGEEERRRREEVLREEIQTLTSKLQELQEM KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSEEGLPRP RSPCSDGRRDAAARVLQAQWKVYKHKKKAVLDEAAVVLQAAFR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS PVQEEAIVIQSALRAHLARARHSATGKRTTTAASTRRRSASAT HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP SLPTKNPPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL GCSFSLEEALSKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAPASIPG CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT GFPTHFNHEPPEETDGPPQAVALVAFLQALEKEVAIIVDQRAWN LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLPLAAKK IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH AEMIQKLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDVEG MKSGKGRPISPVDSPPLSIWICQPTRYAESQKEPQTCNQVSLNT SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR FSPSSSSEADIHLLVSVHKHVSMQINHYQYLLLLFLHESLILLSE NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQANTLK SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS ANPPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL HHIKKMTVE
5497	1821	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPPPFVCFQLSN GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH YYTIGFGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQARKPA STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDQER EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT TTNDRSAPRFS
5498	2434	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYVIKHQNTH TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI QKSNLIRHQRTHTGERPFVCKECGKTFSGKSNLTEHEKIHIGEK PFKCSECGTAPGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QKIHTH
5499	324	926	GFGQIGRGHKITTYPPSPRKEGRKGMAQSQGWVKRYIKAFCKGP FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH WKVRNFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW PPERWQKLESVLPPERLPVQREEE
5500	1978	1286	KPDWRLQNLFPRLYLWRSSRPGFGHLKKRLQMDFKIEHTWDGPP VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPPNELW DYEVVEAPFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS YEALYPVPQHELQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPES DLWLIEKCDI
5501	2927	2226	CRPPVSARVAPCHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSQKTTPVNVIA SGQPSEDMIPTVGPNMRKVTKGNVTIKIWDIGGQPRFRSMWERY CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT LQWLIQHSKSRRS
5502	3	824	NSAFPVWVPERTALTCPLGAAPGSSREAPGIAGPPNSTAMSKL GKFPFKGGGSSKSRAAPSPQEALVRLRETEMLGKKQEYLENRIQ REIALAKKHGTQNKRAALQALKRKKRFEKQLTQIDGTLSTIEFQ RREALENSHTNTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT EQQDIAQEISEAPSQRVGFGDDPDEDELMAELEELEQEELNKKM TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD IKQLAAWAT
5503	216	654	KGVRRRGRVRSDSEDSHLGVPKMSFLLPKLTSKKEVDQAIKSTA EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKNAAIYLVDVDQT AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT SPAGTLGEKPVNS
5504	58	3563	QLSFSFQAPVTPDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL GPTVANPELFRKPGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARPRSIR DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPMIKDPN GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPFWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVZIKEDTPHTALVPEISSDLMAANMEKPFNAAYSIAYHSRPLN DFEXILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILED VRNSPCVSVLLDSGTDASDQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFFRKPGWVVGLGTDGSAMLSCR GGLVEKPQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSNPALARHLQRVARAGGQICHRAKGMLKLMRGFHP VKFCHFLLDPLSIYRPLSEVCQKEIVLITEVNATLGRAYVALBS LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEERPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAVIEEPLQ QYNIIYKSNVEIPKLQPNKPSKELAELVMFNAQISHCYPEYLSNF PQEVKDLLSCNHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL FPELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNFM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			YTMLRDSNATAAKMSLDVMISLYRRNIWNDAKTVNVITTACFSK VTKILVAALTPFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA EKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR FLQPHQREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK NSGEVMTVGINAIKEITARCPLAMTEELLQDLAQYKTHKDKNVM MSARTLIHLFRTLNPQMLQKKFRGKPTEASIEARVQEYGZLDAK DYIPGAEVLEVEKEENAENDEDGWESTSLSEEEDADGEWIDVQH SSDEEQQEISKKLNSMPMEERKAKAAAISTSRVLTQEDFQKIRM AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK PKSDK3TRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKQK NFNMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK
5506	1	1531	FRGDLCGQRGGSAPGEGGSSAWPAPAHPLPERERERREALCPGRS CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWWAVVV LAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGY LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKLV SRRSYEHWEYLTATLISIGVSMPLLSSGPEPRSSPATTLSGLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMPGVNFFSCLFTVGSL LEQQALLEGTRFMGRHSEFAAHALLLSICSACGQLPIFYTIGQF GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL LRVYARGRLKQRGKKAVPVESPVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK VAVADVQFGPMRFHQDQLQVLLVPTKEDNQCNGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIEITSEDRFIQ YANPAFETTMGYQSGELIGKELGEVPINSKKADLLDTINSCIRI GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI FELEAATHNRPLIYLGLKMFARPGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPE
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLHYWVLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELRSKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDPDLEA
5510	96	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKNKRSQAY ADYIGFIILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVVLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVNGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF KPGSLLPIHPVTSG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPYSQKEEVADPQLEVDELLEKDND HSRPDIQVQAKRLAEXLRCDTVVSEISTGQRTVNFKINRELLTK TVLQQVIEDGSKYGLKSELPSGLPQKKIVVEPSSPNVAKKFHVG HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL FGYEEKLQSNPLQHLPEVYVQVNKEAADDKSVAKAAQEFFQRLE LGDVQALSLNQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK SQEVLKLLESKGLLLKTIKQTAVVDLSGNGDPSSICTVMRSDGT SLYATRDLAAAIDRMDKYNFDTMIYVTDKGQKKHPQQVFQMLKI MGYDWAERCQHVPFGVVQGMKTRRGDVTFLEDVLNEIQLRMLQN MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKPSWDR VFQSRGDTGVPLQYTHARLESLEETPGCGYLNDFNTACLQEPQS VSILQHLLRFDEVLYKSSGDFQPRHIVSYLLTLSHLAAVAHKTL QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKVPLPL IEKEKISHNTRRFRPGLPSFDHVLGLPVGNYVQLLAKIDNELVV RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK IGETIFFRGPRGRLFYHGPGNLGIRPDQTSEPKKTLADHLGMIA GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE EIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSPPS PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC FAQETPGKQYKQTIGLDFFIRRITLPGNLNVTLQIWDIGGQTIG GKMLDKYIYGAQGVLLVYDITNYQSFENLEDWYTVVKKVSEESE TQPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG DSVFLCFQKVAAEILGIKLNKABIEQSQRVVKADIVNYNQEPMS RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIYGLWWCTKSILKYICKKQKRT CYLGSKTLFYRLEILEGITIVGMALTGMAGEQPIPGGPHLMLYD YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL MLSNALFVEAPIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL EFLVRNNVLLELLRSSLILLQGSWFPQIGFVLYPPSGGPAWDLM DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS EVGLLKNABREQESEEEM
5515	1572	260	FVRLVGRGDCDPLLSVCLTTMDLYEGLGSGGEKTAVVIDLGEAF TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL KEFIHILVFRHLLVNRDRRVVIIESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHLMALLTLGINDAMVLDCGYRESLVLPIYEGIP VLNCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMPDVGKTQPPLMKRAPSTEK
5516	3	735	NSREPPQAGPGPSPRKSPTASSFLPPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSN DVKLGALGGNTQEVTLQPGEYITKVPVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SEIYVAMRTGSSKMTDVESGVANFASSARAGRRNALPDYQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
5518	3	1375	DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRILLHLIDYLVTSDGKDPEITNLINSTR IHIMPSMNPDGFEAVKXPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDSHITKVIIPEKS
			QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
			KPSLFLFLVSLLHIFFK
5519	87	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG
			GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
			AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117	943	PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI
			SQPGKNEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
			RTKGGKDIKFLTAPRDLLPTTLAFPVSTFVFLAFWILPLYNRDL
			IYPKVLDTVIPVWLNHAMHTPIFPPITLAEVVLRPHSYPSKKTGL
			TLLAAASIAYISRILWLYPETGTWVYPVFAKLSLLGLAAFFSLS
			YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS
			PAKHQLVKNIR
5521	546	911	KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE
			GVSQEAEGNPRGGPNQPGQGPKEDTPVRHLDPEEMIRGVDELER
			LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMNVFGYGSLIWKVDFFYQDKLVGYITNYSRRF
			WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
			AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
			PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEEADEHL
			FALEKLVKERLEGKQNLNCI
5523	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
			KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE
			HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
			RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
			ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
			VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
			FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
			SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
			RDAAEPVEDSAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFSSRFDSG
			NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
			CAETEFENGNRSWFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
			MAPFVRTLPTRPRWERIRDRPTFENTETQFVLSFVHRFVEGRGA
			TTFFAFCYPFSYSDCQELLNQLDQRFPENHPTHSSPLDTIYYHR
			ELLCYSLDGLRVDLLTITSCHGLRRDREPRLEQLFPDTSTPRPF
			RFAGKRIFFLSSRVHPGETPSSPVFNGFLDFILRPDDPRAQTLR
			RLPVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
			IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
			NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWIMPQQSAGLE
			ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
			NMLYPKLISLNSAHPDFQGCNFSEKNMYARDRRDGQSKEGSGRV
			AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA
			FPSRYTVELPEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL
			RAWMLKHVRNSRGLSSTLNVGVNKRRGLRTPPKSHNGLPVSCSE
			NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSPFFHGSRPAGL
			PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
5525	105	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS
			LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
			VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
			SSTSEEPDENSSSVTSCQASLNMGRVKQLTDEEECCICMDGRAD
			LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
			TEDDMANYILNMADEAGQPHRP
5526	3	853	RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
			QVLVPGLPGGGSAKSPFNQWGLQPRSLLLQAARGYVVRKPAQSR
			LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
			KQEQFMKKIVANPEDTRSLRARIIALSVKIRSYEEHLEKHRKDK
			AHKRYLLMSIDQRKKMLKNLRNTNYDVPEKICWGLGIEYTFPPL
			YYRRAHRRFVTKKALCIRVFQETQKLKKRRRALKAAAAAQKQAK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline. Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RRNPDSPAKAIPKTLKDSQ
5527	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSEPKQSSCG
			KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS
			PAKNPSSLFSKEAPKRKAQAVSEEEEEPEQKSSSPKKKIKLKKS
			KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEMTSENLV
			QTAPKKKKNKGKKQLEPSQSTAAKVPKKAKTNIPEVHDQKADVS
			AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDKLDILGA
			AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE
			AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT
			VSDQALLPGDDDAGEGPSSLIREKPVPKQNENSEENLDKEQTGN
			LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
			FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
			YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
			RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
			RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG
			RSLVFANSISCIKRLSGLLKVLDIMPLTLWACMHQKQRLRNLEQ
			FARLEKCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
			RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK
			YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
			EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLPTESQKTK
			YPTQSGKPPLLVSAPSKSESALSCLSKQKKKTKKPKSPQPEQP
			QPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKPE
			YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
			QLMTKCAQTVMEELEDIVIAYGQSDEYSPVFKRKTNWPKRRASK
			FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT
			LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL
			AADKNEILPSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKEIKL
			PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TFRLVSAHLKTRKLYNPEAAERRWRDWDSRQGWLSVKMQRVEGL
			LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE
			KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL
			IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV
			AAAMENPNLRBIVEQCVLEPD
5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQQLVKLTDFGFSNK
			FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML
			VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR
			DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN
			SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
			QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
			ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
			PASLKPTASGRKCLFRVEEDEEDEEDEKKPMSLSTQVVLRRKPS
			VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI
			ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
			TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
			GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
			LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST
			GNAGQVPAVGGIKFPSDIHMADTTTELERIKGKNLKNNVLQLPLC
			EKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	515	GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF
			ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV
			TNVEDLSSLEGYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC
			LGPAPTPATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRKMIYEDETEFCGEELLHSVLQCKSVFDVLDGEEMR
			RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG
			KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK
			GPNDFKLEDFYSASSELFEPYYGPGGIDGDGDITRPENISAFRN
			FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA
			LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS
			RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VVPLEVIKGDHEFTDYNIRSNESHCSLQIKALAKIHAFVQDTTL SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKPFELIQGTEI DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN PIRVKEVYRLEEMEKIPVRLEMKIIKGSSGTPKLSYTGRDDRHF VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS IAPFHICYYGRLPWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ MHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETVVP TVPENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYVGK CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL NLQKLKNSERILTEAKQKMRELTVNIKMKEDLIKELIKTGNDAK SVSKQYTLKVTKLEHDAEQAKVELTETQKQLQELENKDLSDVAM KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN SLEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPSAAPLPTGRAQMSP SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP DAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTPGPLVTDPET HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGPHEDDPF FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPQLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLVQDVMLEN YRNLVSLGLVVSKPDLITPLEQRKEPWNVKSERTVAIQPDVFSH YNKDLLTEHCTEASFQKVISRRHGSCDLENLHLRKRWKREECEG HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG EKNYHCNNSEKTLNQSSSPKQHQENYFLEKQYKCKEFEEVFLQS MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY KCKVCAKPFTCPSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA FSYRSYLTTHRRSHSGZRPYKCEECGKAFNSRSYLIAHQRSHTR EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLGLIDISQAQLSCTGPPAIPGIPG IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEPGEKGDPGIPGNP GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA SSRGNLCVNLMRGRERAQKVVTFCDYAYNTPQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ELEKVHDLCDNFCHRVITCLKGKMPIDLVIEDRDGGCREDFEDY PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS SDQGDGLDTSVASPSSGGEDEDLDQERRNKKRGIFPKVATNIM RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAV KRPPSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG SSASRDRVLARTMIVADSECRAELKDYLRFAPGGVGDSGPGEEQ RESRARRGPRGPSAPIPVEEVLREGAESLEQHLGLEALMSSGRV DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSEINK LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTMCHSLS SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF ESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLL VTPSADILEPSPHPDMLCFVEDPTFGYEDPTRRGAQAPPTPRAQ DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV DTSVLRRAIWNYIHCVPGIRYDDYDYGEVNQLLERNLKVYIKTV ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLLEARMQAALLYAL RAITRTYMT
5544	1895	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEEEEEV ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRKGNLHFIR FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCQK LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF PGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRDIYGGDYERFG LPGWAVASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR MCALNENINQVVPVGNFLRINTIAMRLLAYALDYWSKGQLKALF SEHEGYFGAVGALLELLKIP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPPSPLSNNQEV SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVPLSVT GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH DEL
5546	1592	146	PVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVPT RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTPQVKKYSLVRDVVS SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRRRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5547	1592	146	PVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVPT RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTPQVKKYSLVRDVVS SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRRRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5548	1	2153	DQTGPPETIAFTFPRSTNEPLCPLLLVGFSLPLARALRGNETTA DSNETTTTSGPPDPGASQPLEAWLLLPLLLLLVLLLAAYFFRF RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYREKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKPCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQSEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYSFCYKVVQ DFIDIFSDYANFK
5549	915	256	FEATGGKRLAPKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVBELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVPRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPKPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQNFQYFITVVPT KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH
5551	211	1700	MQRDRTMDYKESCPSVSIPSSDEHREKKKRFTVYKVLVSVGRSE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNPDDPIK QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE DERSSQKLHSTSQNINLGPSGNPHAKPTDPDFLKVIGKGSFGKV LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL EKDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNV AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAPVG FSYAPPSEDLFL
5552	2748	930	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKSEKEKHL DDEERRKRKEEKKRRRERERHCDTEGEADDFDPGKKVEVEPPPDR PVRACRTQPAENESTPIQQLLEHFLRQLQRKDPHGPFAPPVTDA IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNEDTAVEEPVP EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTASEHVL ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT ALSMQNNSVFGDLKSDEMELLYSAYGDETGVQCALSLQEPVKDA GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDQIHL GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPPHVVTPLLESWALSQVAGNP VFLKCENVQPSGSFKIRGIGHPCQEMAKKGCRHLVCSSGGNAGI AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD EANLRAQELAKRDGWENVPPFDHPLIWKGHASLVQELKAVLRTP PGALVLAVGGGGLLAGVVAGLLEVGNQHVPIIAMETHGAHCFNA AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL PPSLTSVVVIVCGGNNINSRELQALKTHLGQV
5554	166	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLPQ VHTFEIFQKELNESENSVFQAVVGLQRALQGDYKDVVNNKESSR QRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLQML DEILEDVRKAADRLEEEIEEHAFDDNKSVKGVNFEAVLRVEEEE ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMPGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVPISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQNGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEPSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL
5555	212	1425	LSLRTRETPAPPRCEAASQGRVGWRADAAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMPGGTPRQQDRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGSPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQQSVQK VYNGLQGY
5556	5835	3346	RTRGMSKNCVPMEFEEYLLRNFQGTFYLLQKITKDNNAHTVKSR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA LRLVDKAQVLVCRALSNILLLDWPNLPENEQQWPVRSINHASLI SALSRDYRNLKPSAVAPQRKMDLDDTKLIIHQTLSVLEDIVENI SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL TLFRGLRVQMGVPFTEQIIQTFLNMFTRBQLAESILHEGSTGCR VVEKPLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS PDVKABLFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVTD RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKVV ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP AMSSRGLFKNLGIEAVPWTADIPLKVVGMPPSRGEKRALWKLAY DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYIHVLSVI WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY LIQMIPRQNLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD YTVTNLAGGPKPYSPYDSQYHETTLKGGMPAGQLTKVGNQQMFA LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA SLQPGISEDLKKVKDRMGIDSSDRVDFFILLDNVAAEQAHNLPS CPNLKRFARNIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKNPP FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF LNAMSVYTLSPEKYHALCSQTQVNEVGNEE
5559	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLG KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG PTKPSEGPAKVEEEAAPSIPDEPLERVKNNDPEMTEVNVNNSDC ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG GKTEMEIAKLLKENTTLLKLGYHPELAGPRMTVTNLLSRNMDKQ RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPK PSPKNSPKKGGAPAAPPPPPPPLAPPLIMENLKNSLSPATQRKM GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
5560	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGPLSAEECVAM QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT EPLGRVLGVKIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG SAPGTSPLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL SDRSRQAYTPHLMEASGTTWSPENWLQPTAELPFPQLYT
5561	2175	1775	CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QLLAPTVPSAPGVMNFGNPGVPVAPGALPPPPPPHLVPNTQAPS QVVGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS S
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT INSPGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT INSPGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC VPLTWRCDRDLDCSDGSDEEHCRIEPCTQKGQCPPPPGLPCPCT GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP
5565	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVPFGCAFIAFGPA LALYVFTIATEPLRIIPLIAGAPFWLVSLLISSLVWFMARVIID NKDGPTQKYLLIPGAFVSVYIQEMFRPAYYKLLKKASEGLKSIN PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH GDSPQFFLYSAFMTLVIILLIIVFWGIVFFDGCEKKKWGILLIVL LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS LKLCLLCQDKNFLLYNQRSR
5566	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPLYYGYKAVKT KNVKEYVRWMMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV IWLLSPYTKGASLIYRKFLHPLLLSSKEREIDDYIVQAKERGYET MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSPSMHDLTTIQG DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA EGPYSDNEMLTEKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK RPQVYF
5567	1554	233	EFLSGGVSPDLANEDGLTALHQCCIDDPREMVQQLLEAGANINA CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDQD GWEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE EVRAKLLELKHKHDALLRAQSRQRSLLRRRTSSAGSRGKVVRRV SLTQRTDLYRKCHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPEGPETAEP GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
5568	1731	587	AEDRQPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFPTALL SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIPVYE NPISLLCGAIIIWRFAGNFERTVGTVRHCPFTVIFAIPSAIIFL SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVPG MVVPSVLVPMLLLGASNLIPQTSPLSNVCGLGIGLAYGLTYCYS IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAQSRKL NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP VNSPGTVYSGALGTPGAAGSKESSRVPMP
5569	2	835	QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKLLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG PMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEPVVKFYGPQGT PYEGGVNKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEEYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED EAQDMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEPVVKFYGPQGT PYEGGVNKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEEYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED EAQDMEL
5572	2802	2085	RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV RWGRRGLGAGAGAGESPATSLPRMKKRDFSLEQLRQYDGSRNP RILLAVNGKVFDVTKGSKFYGPAGPYGIPAGRDASRGLATFCLD KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE EPSEYTDEEDTKDHNKQD
5573	2562	219	VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET GSGKTGAFSIPVIQIVYETLKDQQEGKXGKTTIKTGASVLNKWQ MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE VSCHDQGLCRVGWSTMQASLDLGTDKFGPGFGGTGKKSHNKQFD NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK SQHSGNAQVTQTKFLPNAPKALIVEPSRELASQTLNNIKQFKKY IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL APTVQELAALEKEAQTSFLHLGYLPNQLFRTP
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
5575	456	766	LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWPWRMRLLRRRHMPLRLAWVGCAFVLFLFLLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPSA QQTLPSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQX SKWTPLETQEKEEGYKKHCFNAPASDRISLQRSLGPDTRPPECV DQKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK EIILVDDASTEEHLKEKLEQYVKQLQVVRVVRVQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI VTIDLNTPEFAKPVQRGRVHSRGNPDWSLTPGWETLPPHEKQRR KDETYPIKSPTPAGGLFSISKSYFEHIGTYDNQMEINGGENVEM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQVR LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLQLREQLHC HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNQCLDVGENNRG GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG LGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA MAPCNPSDPHQLWLFV
5577	3	1275	RNSDCSCGEISVHCLPWVLPILLDLKVESSMFCPLKLILLPVLLD YSLGLNDLNVSPPELTVHVGDSALMGCVPQSTEDKCIPKIDWTL SPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLL QDVQEADQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV GGLIQMGCVPQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIV GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIK EKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPV WPSLRSDRNNSLEKKSGGGMPKTQQAP
5578	3	783	AVESMASPGAGRAPPELPERNCGVREVEVWDQRVQGAADSAPYD WFGDPSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV TSVDYSSVVVAAMQARYAHVPQLRNETMDVRKLDFPSASFDVVL EKGTLDALLAGERDPWTVSSEGVHTVCQVLSEVSRVLVPGGRFI SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGPHFHLYLMHKGGK LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
5579	3	1540	RNSGLARGASALARHGGGLACGVGWDCGACASRCQGVMEGLLTR CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK ELLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTVSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTPYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKQSKEQAASELIGQQLYDHITEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAFLTKDGVMDLLTPVQTV
5580	1681	450	ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSCRMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELPRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SFDKTASVPLLEKDRLVKENNYRCHGDSVDQLCWIPGNPDLPVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLPGLPNDS
5581	54	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVPACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW
5582	5775	2739	IITNNNNVIIPLVIAYHLSGSAQARGERGPAERLMERQKRKADI SKGLQFIQSTLPLKQEEYRAFLLKLVQNLFABGNDLFRKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY SKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTNPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPBLDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK RDILLGRLRSSEDQTWKRIRPRPTKTSPVGSYYLCKDMINKQDC KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT IAKLLKEHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHEVRYGCL REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR KDMLLCPRDDDPGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIP PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA
5584	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIP PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEESIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKQQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5587	1768	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CVAVYKDGRAGVVANDAGDRVTPAVVAVSENEEIVGLAAKQSRI RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF DPGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE TLAQYLASEFQRSFKHDVRGNARANMKLTNSAEVAKHSLSTLGS ANCFLDSLYEGQDFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ NGFTADDINKVVLCGGSSRIPKIQQLIKDLFPAVELLNSIPPDE VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS PRRPRSPPSSPLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF *RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDPAERGEAWALM* KEIEAAGRALQSVHAVPSAPAVPSGTGQTSAELEVQRRHSLVSP VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGP TFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARV TLLRLRQSPRAFIPPAPVLPSRDNSIVDSASVPETPLDCEVSLW SSWGLCGGHCSRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPQSGLDLADA LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY QQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE PPPPPEPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG DIGNKVSEQLQAKNPMKKEAKPSATGKVIDKKLPKPLEKVPNLV PVPVSEPVPEPEPEPSPEPEPVKEEKLSPEPILVDTASPSPMETSG CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL RQLEEEQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQET MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEI GDFAPVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESRDWNQKDLLSALVLTTVNCLPTPIMAKSAEVRLAIFGRAG VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTHVKQAINK MLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR SLDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENIGHLTELQ EFWWNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MLALPSVRQIDATFVRP
5594	3	1113	HASGGRAANNAAERGACQQQSQEMMEVDRRVESEESGDEEGKKH SSGIVADLSEQSLKDGSERGEEDPEEEHELPVDMETINLDRDAE DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTBLQ EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV MLALPSVRQIDATFVRP
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAPGD VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL LDQKHVQDIVPQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG GSKCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVVKISFIFP NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV KGEGEYTHIGQTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAVLSLSP VPVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIQEPR PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTNNA RPLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW FEYTVTRAEARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPERFVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVPGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLBE IKCALCSPHSQSLFHSPERFVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE EDNCPEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCPPTHVSRRIPVLSPKP AVAPPAPPSSSQLCRYPPACKKMECPFYHPKHCRFNTQCTRPDC TFYHPTINVPPRHALKWIRPQTSS
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE EDMCPEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCPPTHVSRRIPVLSPKP AVAPPAPPSSSQLCRYPPACKKMECPFYHPKHCRFNTQCTRPDC TFYHPTINVPPRHALKWIRPQTSS
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQQILNMF
5603	1	565	FRGRTPISGGERGCAQYPIPATPARSGENRTMPGAGDGGKAPAR WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS CPGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA TIFLQVVDRRMQ
5604	1	1506	EDIYFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYESCSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN
5605	35	1821	SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRNLTEWRDEATRSRHRTRPVPQ KALRSLRRYPLPLRSGKEAKILQHPGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYHP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELAGEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT
5606	3	1099	GRGRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVTQTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQQGPQWSGCSDNIAYQ VAFSQSFVDVRERSKQASSSRALMNLHNNEAGRKAILTHNRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG SSRALVPRNAQPKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKC RQCQRLVELHTCR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRV QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
5608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV RIQTEPKYTGIWHCVRDTYHRERVWGFYRGLLLPVCTVSLVSSE VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPEP KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL QADGQGQRRYRGLLHCMVTIVREEGPRVLFKGLVLNCCRAPPVN MVVPVAYEAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS GTGIHIDPLGTSAWNALVQGHKRWCLPPTSTPRELIKVTRDEGG NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG WWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSDSD SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS R
5610	54	1196	LERTPASADNAWTKYQLPLAGLMLVTGSINTLSAKWADNFMAEG CGGSKEHSPQHPFLQAVGMFLGEFSCLAAFYLLRCRAAQQSDSS VDPQQPFNPLLPLPPALCDMTGTSLMYVALNMTSASSPQMLRGA VIIFTGLPSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ VGQQPLIAVALLGNISSIAFFNPAGISVTKELSATTRMVLDSLR TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG ELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPE KLTAFKEKYMEFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKM ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP KPVGPPPERDIASLP
5612	1	721	ASRDGYMDATIAPHRYPPEMPQYGEENHIPELMQAMWLCKHLNS SLLTLENLILNEPSYTATEARRLYLQRKTVPSALLVQLIQERLA EEDCIKQGWILDGIPETRBQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGIYHTTFDWPPESEIQNRLMVPEDISELET AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKYSGWFRSILSD KTSRNLFFFLCLNLSFAPVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIPVFKHGGH GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVVSVIPLLRESVGILMQR TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQQQETQNER APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC EDNYVQATDKRKALEETMAPTTQALASVAYQVGNLAGHTLRMLD LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVBVP QRPPTLEELSPPPPDEELPLPLDLPPPPPLDGDELGLPPPPPGP GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SDGWCEGVSSEGTGFFPGNYVEPSC
5615	9	1558	ALGRRRPGDPREMEAAATPAAAGAAKREELDMDVMRPLINEQNF DGTSDEEHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAPEGIGVVLPLENQ MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDEIKGSITLN LPQDVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV EEIIYPTPKVVAGTPQSPPLNNLNSTCLTSGLK
5616	1	719	DDPVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV YAPLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG TCEAAGKSPEPKDYDSTCVPCRIAGRQDPGTELLHCENEDLICF KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV YRVNSYWFITADHLIEKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES LFLNSGGDSLKSIRLLSEIEKLVGTSVPQLLEIILSSSILEIYN HILQTVVPDSEDVTFRKSCATKRKLSNINQEEASGTSLHQKAIMT FTCHNEINAPVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTQKMELH VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY SGKVKNEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNGG EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW KHSCGKPLFSSPQCCSQYICIGCVDGNLLCFTHPGEQVWQFSTG GPIFSSPCTSPSEQKIPFGSHDCFIYCCNMKGHLQWKFETTSRV YATPFAFHNVNGSNEMLLAAASTDGKVWILESQSGGQLQSVYELP GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSPLGHCSVL LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGNQPPLGP TVGLRPGLLGERQRGALRAGDPQCQCPLPATVRRDLGVPSPWAA ECSPPATP
5620	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIQCAMSG LIADAKTLIDKARVETQNHWFTYNETNTVESVTQAVSNLALQPG EEDADPGAMSRPPGVALLPGGVDEKGPQLFHMDPSGTFVQCDAR AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLILLKQVMEEKLNA TNIELATVQPQQNFHMFTKEELEEVIKDI
5621	3	819	VVEPVEVTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF MIMLGDKEKTFCFLHQFSRLLTSAPLWLPRLHISSYLPNDTVES GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLQWIT QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR NIRLQST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKANY PGTFYFQFKNLWEANDRNETWLCFTVEGIKKRSVVSWKTQVPRN QVDSETHCHAERCFLSWFCDDILSPNTKYQVTNYTSWSPCPDCA GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EIMDYEDFKYCWENPVYNDNEPFKPWKGLKTNFRLLKRRLRESL Q
5623	3	954	FLPPFIRADKISRNGQWLFTPTTPFPPANKALPGWEGIVPACPW RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGFAPALVSCRRELSLSAGSLQLERKRRDFT SSGSRKLYPDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1180	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVPFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGQKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVPFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGQKKKIH
5628	75	1455	VAGAMASKCLKAGFSSGGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWPGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVSAVAMAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN FAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ADEDINKRPLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV NQFALASHFFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP EVTALKVPE
5630	1194	278	GFWAIAQTCAHHLPPGSPWLVPASPWRLFENSSFGYRTLTVALF TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM NSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT LFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSC LAVLDLMSRGGNIPHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAVWRRLPQAFRP
5631	1053	290	SRVDDFVRPEPSRAEPSRSGRRRPARRAATMSVFGKLFGAGGGK AGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQELTAAKKHG TKNKRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTN TEVLKNMGYAAKAMKAAHDNMDIDKVDELMQDIADQQELAEEIS TAISKPVGFGEEFDEDELMAELEELEQEELDKNLLEISGPETVP LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD FTPVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGF NRQVVRDNPDFWGPLAVVLFPSMISLYGQPRVVSWIITIWIFGS LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE VVSTLIKLPGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY FLSLYTGV
5633	771	460	QGCSKTMSVGRPPVRSSEPMEQLLSSHLHQVPPFCCPTVVCLCN CLPENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL LLLLLSGHRPWGSSMV
5634	1446	855	PRATGRIRSRAAASRPRAGAGASGAEPREGRERGRLSGRRAPAM ARNTLSSRFRRVDIDEPDENKPVDEQSEAAAAAAEPGPDPSEVD GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK ALAVGGLGSIIRVLTARKTV
5635	3	943	DRGPRSTATDIGRARVSPWRFPLDPGVKNSNVQISGERRRFRTL RSLFHPFPVTRSGAPRAVLVGSSNPAKMVAPAVKVARGNSGLAL GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE EKYVRELKKTQLIKAAPAGKTSSVPEDPVISKFTNMMMIGGNKV LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA HYRWW
5636	2253	1143	LEDTICQHPDAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG LTDVRAKVTGPSEGVVDSVKGGFSSFSQATHSAAGAVVSKPRBI ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK HWDALFSYVERFFSSPR
5637	948	2532	MSPCGARANAKMMAAVNGGTSAAAAGHHHHHHHHLPHLPPPHLH HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMLNPG QQQPYFPSPAPGQAPQPAAAAPAQVQAAAAATVKAHHHQHSHHP QQQLDIEPDRPIGYGAPGVVWSVTDPRDGKRVALKKMPNVFQNL VSCKRVPRELKMLCPFKHDNVLSALDILQPPHIDYFEEIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK CCFSTSTGRVYTSDFEPVTNPKPDDTFEKNLSSVRQVKEIIHQF ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE
5638	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5639	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVS IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAP GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPK LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT VPESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLPTFHGLLHFLDGSIQKLIQA EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY TWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT KANELLFLHVYEFDIVMFPKNVRCSTCDLRKPARSKHCSVCNWC VHRFDHHCVWVNNCIGAWNIRYYFLIYVLTLTASAATVAIVSTTF LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLTFPRIVFM LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVWHRRGVGAGAIAKKKLAEAK YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC LALKHRNGGLITLEELHQQVLKGRGKPAQDVSQDDLIRAIKKLK ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTVS EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF TDLYSQEITAEEARERALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHFGWTVAGQFQEKKRFTEEVIEYFQ KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW RYVPINVVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
5645	537	799	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ
5647	288	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QRVLPLPIPTPAKMGATKEEREDTPIQLQELLALETALGGQCVD RQEVAEITKQLPDVVPVSKPGALRRSLSRSMSQEAQRG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM APQSLPSSRMAPLGMLLGLLMAACFTPCLSHQNLKEFALTNPEK SSTKETERKETKAEEELDAEVLEVFHPTHEWQALQPGQAVPAQS HVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS ALAKFKEGAEMESSKEDKARQAEVKRLPRPIEELKKDFDELNVV IETDMQIMVRLINKPNSSSSSLEEKIAALFDLEYYVHQMDNAQD LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEAELT QEMSPEKLQQYRQVHLLPGLWEQGNCEITVHLLALPEHDAREKV LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE DEGYFQELLGSVNSLLKELR
5649	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENPDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENPDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*EAHAKQPASESPRV*EGSGWEQPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAQSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSNAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRDSSPS
5652	735	343	HHKKVQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
5653	66	1401	RGHLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGPLTAPL CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEPVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ GWLLELQFRRRSLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK PTVHQECEQGFDRKASHSGYPKTHTGYKPYVCNEYGTPFSQSTY LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK THAANV
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL NWKPFVYGGLASITAECGTFPIDLTKTRFQIQGQTNDAKFKEII YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR PRLHRSQVKSLRCV*KEQIA**/MPSLLISTLISKYIYYAADVL EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH AVHPLTPLITYSDEHPSPGSHPSHIPSDVNSKQGMSRHPPAPDI PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAPFHSGRLQRSLTKDSAGCFSQCRSRAM LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLR PSNMNAFMENLKKNIHLRTSYSELVGFWSVEPGGRTNKVFHIWK YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERAINAHVNLGY TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG GVRESVNYL\VSQQNM
5657	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAAEMNGEEEESEEER SGSQTESEEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEKL FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE RTMLSDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA LKVIPYLDSYHFSKLPSRLEGGASLRLHTALPTKVLENVEGLPS PGSQAAEDLQQDINAQSLSKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN GDL
5659	2	696	WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\ EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRPLCGVVEGFYGRPWVMEQRKEL FRRLQKWELNTYL
5660	229	853	PVTHWAPSELPMPLLINLIVSLLGFVATVTLIPAFRGHPIAARL CGQDLNKTSRQQIPESQGVISGAVFLIILFCPIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC PYGTYPREPPLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASPLAEAPLPVTVRGSGL AGMAVTCDPXAFLSIC?VTLVFLQLPLASICQN*GTDSCASRGK ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRPCSSA PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLYKSPSKR QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT NVLGSILRIRSEATAAIHSFPKDSGFVHIHTPIITSNDSEQAGE LFQLEPSGKLKVPEENFFNVPAPLTVSGQLHLEVMSGAFTQVPT PGPTFRAENSQSRRHLAEPYMIBAEISPVDSLQDLMQVIEELFK ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNPLIISYTE AVEILKQASQNFTPTPEWGADLRTEHEKYLVKHCGNIPVFVINY PLTLKPFYMRDNEDGPQELEGSVA*HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGWCPLKGASGCPGAERSLL VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPPVICSHPP QDLWAEQDIKDSPQEAILKKYGKYGHANPQLQKGCKSVDECKVH KEHDNKLNQCLIPKKKK
5664	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIYLLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE ETEVEGKRKRGRPGRPPSTNKKPRRSPGEKSRIEAGIRGAGRGR ANGHPQQNGEGEPVTLPEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPPNSSHPDEVKIAALVPYSCIFII GLPVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPPRM PYYAKDEWPPGEYPCQILGA
5667	1	695	MPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGBP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQ
5668	691	894	CSPLFCIPDLPLQPLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPPIYLHARKRRGEIGD ADSRPNDRYAHKSAQLYFLYPVCWIPQDVYYPTIKEKNHFFFPK ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL NSQ
5670	3	373	SSECLTMAWIPLLLPLLILCTVSVASVELAQPSSVSVSPGQTAK ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG STSGTTVTLTISGAQVEDEADYFCYSATDNPLWVF
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLVYRIVEGKNLPAKDITGS SDPYCIVKVDNEPIIRTATVWKTLCPFWGEEYQVHLPPTPHAVA FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP NPPSHSETSPLGSVWSPAQGKPFLLSPEAGATPCTPGLCSAACS QAWLLLPLP
5673	327	696	ITVADQISHWSAGRYKNRTRIPECIHSSAATTLAGPHTMEGESV KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAPQHLHTDSDTEGFLLGEVKGE AKNSITDSQMDEVEVVYTIDIQKYIPCYQLPSFYNSSGEVNEQA LKKILSNVKKNVVGWYKPRRHSDQIMTFRERLLHKNLQEHFSNQ DLVPLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKIN EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA QIQAARENKIQKDPQENIPLCQALRTFFPNSEPLHSCVMSLKID MFLKVAVTTTTISM
5675	80	753	EGSRRGPTRLARLSARAGRLHFPPGPFSSRLYHFRGVSECRRPPG KSGVPVSAPGSDGKWWEERPGMPSLMASCCGWFKRWREPVRKVT LLMVGLDNAGKTATAKGIGGEYPEDVAPTVGFSKINLRQGKFEV TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SEMLRHPRISGKPILVLANKQDKEGALGEADVYFCLSLEKLVNE HKCL
5676	2	930	FVSSPPPRPVQPARPGGPGLSGRRSLLCQVASTPAHVGVMRSPV RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM LLGPGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTPPA MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN WTYVFYPPGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH RKHAGPIVSVWHRELRKAKSNRELTFLYLANDVIQNSKRKGPEP TREPESVLVDAFSHVAREADEQCKKPLERLLNIWQERSVYGGEF IQQLKLSMEDSKSPPPKATEEKKSLKRTPQQIQEEEDDDYPGSY SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	SSSPPSSTPSLPLPFVLLLGQLRLQLLWGTAHLSGAGEAAPCPG GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIEE SLAEFTEQFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGEE PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE DDAEVQQECLHKPSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH FDPRKADSIPTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLQNRNSHTPLESLIHPQPSVKGFGIMFGKKKKKIE ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA RQTRPQRLRKEAARPPTPGSCPGGTGMDGKKCSVMMFLPLVFTL FTSAGLWIVYFIAVEDDKILPLNSAERKPGVRHAPYISIAGDDP PASCVFSQVMNMAAPLALVVAVLRFIQLKPKVLNPWLNISGLVA LCLASFGMTLLGNFQLTNDEEIHNVGTSLTPGFGTLTCWIQAAL TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLPGSYGL PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYQ GASVILPCRYRYEPALVSPRRVRVKWWXLSENGAPEKDVLVAIG LRHRSPGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLNWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKVRGAPCEAKIKT AKRLVKVKVTPRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPGPHTTGIPHPAIVTPQ VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE RQLHMQLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTWWQVNITLLDINDNHPTWKDAPVYINLVEMTPPDSDVTTVVA VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP RNDPLINSSSGVVVTTTELDRERIAEYQLRVVASDAGTPTKSST STLTIHVLDVNDETPTFPPAVYNVSVSEDVPR\GSGWSG*AARN NDVGLNAELSY?ITGGNVDGKFSVGYRDAVVRTVVGLDRETTAA YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPELLPGP\SSS LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT SGCRMPSTSASE/AAGGQGACTHAKGSETPPPAS?QTSEPAPSP LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG PPVLPHVCTPSLANPQP\AVGPEASSLPLGVSGIGMSA/SAPIS SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP VLDI
5688	1	420	LTKWDLFGNCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLPF *SHMIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV LRVEKTPAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID DGYIPAVF
5689	1504	3	HELSGRHISMVSGNTCNWHPGGHSPGGGGQGEITSKDRGHIPAL IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPPQPCEGPRSTSRG GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQPWDQHPHS PGEHRPSG\SPLPACPPRAW?KAGAVASATGTG\PQLPGSRGKQ KLPRTREPPLLQAGWAVRKP?WSEAKEGLGQAGRPSGMDSSAS\ ?QTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF GQELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRHPCSPGAEAAPWQTGGPAID GAWRTSVSALRRGATG/APCSPGARAAPWQTGGPAIDG\DGELP *VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQDPEP DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERAHVRH PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS SLSLLGP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP* GNFVR*LLLMP/GVA*RHQTSPFLGPSLGENGGQWDSGNLPGTP KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGRQGVRINCLRVGE SEMWGPYSAPRPGTVFLSSFLSPASSEH\PEGSSSFNTPFPPAG PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGVNYEQMAKRGKKLVELPYTVKGMDVSFSGILSPIED VAHRMLATGECTPEDLCPSLQVMQ*KTGTESNG*RFYIVEQN*S GDAPLIFSPYLSLTGNCGPAMLVEITERAMAH\CGSPGGPSLWG GVGVYVLLESVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLERGPPT*RGSHPL\QSVPCIQK PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ RLNLPVMGATRSNLQPPKVAVPGPTR*RDQDSKQDFSSKPLQS VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP *QAGPPSSLRPP\SRRR*APEWPKRATQSRCRGLSAPPWPWPAA RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS PEAIVWRSSRFPLWFPLRCCFMVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEEKAPKKLBYDSGDSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI
5695	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLPGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDPPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLPGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA
5698	2	666	GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSPKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ
5699	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DERPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEQ\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GNQPRRPGFAGRAALPGPPHPPS8*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG
5700	923	597	NGHKGVWEINIY*RRSNIHKN5K8ESHLNQDHSFPPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD E*CSIASSLIKAILRVSVLSE
5701	59	410	IFEKICSDTQEPISPEINPQICSWLIPDKGAX/NHATGKDSLPN KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5702	3	1517	ETPVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSH ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLABALVTVTN IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA PVSIEAGSAVGKTTSPAGSSASSYSPSEAALKNFTPSETLIMDI TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP PTATPTTARTRPTT\A*VQVKMEVSSSCG*VWLPRKTSLTPEWQ KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR GCCP*PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	HHKDSRSQQLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS RILRWHP*HTAAR*PRWRRLPSSHRNTRHLGVLRVQDKS**VSL DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVPPARPVS ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR GSWETAPGS*NCPWL*AARWTGWRTASGASAGLGRAADRPSAWA RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA AGWPRHSPHDTQTPEP
5704	23	562	SDYEFDSPVWDDISQAAKDLVTRLMEVEQDQRITAEEAYSHEWI SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP
5705	23	562	GDYEFDSPVWDDISQAAKDLVTRLMEVEQDQRITAEEAYSHEWI SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE SPQP
5706	1161	610	QLGRPXAQDTVAIRKVKEVFSTGAMRHVVILFTHKED*GQQALD DYVANTDNCSLKDLVRECERRYCAFNNWGSVEEQRQQQAELLAV IERLGREREQSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVPLLLCSI LFFIIPLF
5707	28	609	GSPAPTPGFRRRPGRGTPSPGTRHHQGRAEPEVDAPERAPLRH* MFAIQPGLAEGGQPLGDPPPGLCQPELQPDSNSNFMASAKDANE NWHGMPGRVEPILRSSSESPSDNQAFQAPGSPEEGVRSPPEGA EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPEPACG TPRGPGPPEPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL RVSPASGGPRKEGRQGSGG*AGGGGP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG RAAG*CSNQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS* AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA PPPRPEPPPPPARRP
5709	2	2031	ITLCPLPQTEKCLNVVTEAATPLGIYYLKARVEAGGLKELETSWG LHQIVVRNGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS I.IHNNVCMAAVPVDRAGEWKLGGLDYMYSAQGNGGGPRKGIPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFM SNRFVETNLFLEEIQIKEPAEKQKPFQELSKSLDAFPEDFCRHK VLPQLLTAPEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLQAKDEQGPI RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRD?FAPSRVAGV LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS. FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA GAKLPGATS*RYTAGQRV
5710	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK VLQMLDTVRVLFSKGPFIAIPASDPHIIIKAINQNLNSVPSGFK \LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA QILQGYRKKLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAPTSTPVLFYPDSAQPFIVKSESS SQIAKAVLSQQRPSLFHECAFHFFS*SLQRHTINLDQGIF*LLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL QIL
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP ETVIDLLNKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/ TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL HKIFHLW\DTLLLGEFLPPILYWE
5713	634	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHNLCGVSFH
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSSGPKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS HYSSFGSSGGSGGGSMMGGESADKATAAAAAASLLANGHDLAAA MA
5715	131	1979	ESASQQKRSKCLYILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH
5716	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT
5717	44	1489	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD EGPGALVLESDLLLGQDLEFEEEEEEEEGDGNSDQLMGFERDSE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GDSLGARPGLPYGLSDDRSGGGRALSAESEVEEPARGPGEAAGE RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTPV SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG Q\CGVKGRASAGLDQNHCOS/SLFPNTCRGCGQEELERGEGSRLG AAMCGRCMRGEAGGASGGPQGPSDKGFACSLCPFATHYPNHLA RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
5718	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT S**STADPLML
5719	48	428	ELNNGPFQNPLCNGGNLAVTGSWADRSPLREAASQGRLLALRTL LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK \RCT\YYB\TCGGTYGLQMWSVSPQDVAQKVVAL\RKKQQ\LAI GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD Y\SSSVPSTPSISQRRLRIETIAASSTPTPIRKQSKRRSNIPTS RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM QHPASG
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQPKRPIENVRRHIGCVA VPYAIAGGLPLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI SFMFSYILLTMCRNLITFLRETPLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPCGAAQSPHRGRRHGGGGAGLPPPRSPRFPP QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA PPPPPHLGALTAGSGEERQSQPRABTLRLGRGAPLP\PRAERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPCGAAQSPHRGRRHGGGGAGLPPPRSPRFPP QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA PPPPPHLGALTAGSGEERQSQPRABTLRLGRGAPLP\PRAERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK KGWLTKQYEDGQWKKHWPALADQSLRYYRDSVAEEAADLDGEID LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQEAELGEP DPEQKRSRARE\RRREGRSKTFDWAEFRPIQQALAQERVGGVGP ADTH\DPWRPEAEHGELERERARRREERRKRPGMLDATDGPGTE DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWHQVETTPLREEK QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ NRLLQDQLRVALGRRQSAREGYVLQATCERGFAAMEETHQKKIE DLQRQHQRELEKLREEKDRLLAEETAATISAICAKKNAHREEME RELEKSQRSQISSVNSDVEALRRQYLESLQSVQRELEVLSEQYS QKCLENAHLAQALEAERQALRQCQRENQELNAHNCELNNRLAAE ITRLRTLLTGDGGEATGSPLAQGKDAYELEVPSGARPCLTQLC TQEPQGSAANPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
5725	3	1049	VNGHSEETSQSPNRTEPHDSDCSVDLGISKSTSDLSPQKSGPVG SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLR/PTSAVDG KNIVRSKAATLLYDQPLQVPTOSSSSSDLISGTKAIFKPDSNHN PE/GAKYNKRPHRWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR TSP
5726	2	486	SRSLSMWWNSGLPASSHSSKLPVTVGPSGCVKRLRLHGRPLGAP TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT GLIFHLGQARTPPYLQLQVTEKQVLLRADDQ
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG NAIRAGVNPGRGPASPFWDLSLPWDLNPPPTDHAPGAPDFPAVE GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED EPPQVPEAGEEDAVPABEGPGGTPETQADQVRERPEAHLAEGGA KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWNQQDAALGRATDSKEPPGEL CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK QLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRV KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE CDYLQGFQILCDLHDGPSGVGAKAAELLQDEYSGRGIITWGLLP GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR PEPPVSFPYLHYDATLPPHCSAILATALDTVTCS\YRLCSSPVS MVHL\ADMLSFCGKKVVTAGAIIPPPLAPGQSLPDSLMQFGGAT PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA LHACTTGEEILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVPHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGPGHRPHKDLWAT KIETEGFWERPPNFENQGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCVMRKPPRRPKKRRQG/CALPQGCLTFKDVAI EPSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLPEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGPEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS ?DEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIPFIVPTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAPEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRNW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL
5735	2	540	FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRNQRREISGNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLMY LKILT
5736	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TARLSVTPPNLLPTVSFPQPDLPDNPVYSTTTEKLASDLRANKN QES**ILPDSGIPIP*T*TSYLQSTTHLRRAKLPQLLRR
5737	290	1041	KACLHLLSSPLTSNFLPNPLLPDSLYSVEARSQRANLQPCRRKR LQTLMRLAAGFQYSSHKDPSLSAKEK:TDYHNEARGPWPGWVG* RTADGSCGRGPDGAHMPGPKSSSWRASRLLPGLGGSHHLDAYVG RDLECGTPAPLQLEIPPQPRPGHPAPIPTGQAGPRDSGPGASP*V ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
5738	8	460	DTLSLNCTLPETLPMTPSF*LSFL*PPGLARAKSIPTKTVSNEV VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT ATQPAAFLFTVPSLPRGVGCIFYEMATGRPLFPGSTVEEQLHFI FRILSEEAWALCAVETHR
5739	1	1222	SFQRRGIRWNVHTLHPHPRAVWAGICRGHGS*ALLGRARAPALC FPTLLEFLESL3PDLPALRAMGLHLWAAGPGTHPAGISDLLAEV SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQQHCMATS PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF LQEVNVYGVTV
5740	285	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A YVYERVYN*NISRMVKALEQKRHPAGLSSSMALQLNPCLGMLMA LQSELHKLYDEETQSWVSGSACGGYP
5741	1	650	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD YVARPGDKVAARVKAVDGDEQMILAEVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCFYRALIHAPPQRPQDDYSVLPEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK
5742	2	362	TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG
5743	2	415	GKTPEGIDAIEEIEIDLEETEREIESPQENGLEEVKPLQEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE
5744	3	703	TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQNTTIA VFTTANTCLSLTPSTLPEEATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL
5745	1400	599	GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEFKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLNDQSI LGF
5746	3	821	SFASGRLTPSSPAPDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGNQATPATEGLARPQAPSSSAPRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPQPEPRSVPQPEPEPQPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV
5747	2	1328	DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE ESSSPVRKESSRGRHREKEDIKITKERTPESEEENVEWETNRDD

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPXSSSASKKDRKTS AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR RE
5748	934	473	SEGPQVFYKGLAPTLIAIFPVAGLQFSCVSSLKHLYKWAIPAEG KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGPEHARAA FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM PFSYEFFCNVFHCMNRTASQR
5749	532	1	GPPVDPRVRGSTLSLARRPKGMIRSGSFRDPTDDVHGSVLSLAS SASSTYSSAEERMQSEQIRKLRRELESSQEKVATLTSQLSANAN LVAAFEQSLVNMTSRLRHLASTAEEKDTELLDLRETIDFLKKKN SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLPVDDSGRVLAIQF HLEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT ILNDIKLADCEQFQMPDLCA3EIAIILGICTNFQKNNPVHTLTE VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL GCTSSALQIFEKLEMWE
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALVAPRSAEPNALA FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPVKRRDREA LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT VERENELRHKNEMLRVETEARARAKAERENADIIREQIRLKASE HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV AERQHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAFPGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEIAEAIASREQEVLQGWKELLSACEDARLHVSST ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSGDMPI RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI ASNAAATVSRERQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEPKVHRVRFFNYVPSGIRCVA YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFPPGHESRATEALC WAEGQRLFSAGLNGEIMEYDLQALNIKYAMDAFGGPIWSMAASP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SGSQLLVGCEDGSVKLFQITPDKIPV
5759	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR MARSSPYPTDVARVVNAPIFHVVNADDPEAVIYVCSVAAEWRNTP NKDVGADLVCYRRRGHNEMDEPMPTQPLMYKQIHRQVPVLKKYA DKLIAEGTVTLQEFEEEIAKYDRICEEAYGRSKDKKILNHIKHWL DSPWPGFFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL NGQDVERGTFSHRHHVLHDQEVDRRTCVPMNHLWPDQAPVTVCN SSLSEYGVLGFELGYAMASPNALVLNEAQFGDFHNTAQCIIDQF ISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLQMSNDD SDAYPAFTKDFEVSQL
5760	1	1221	VRDITSDSLSLSWTVPEGQFDHPLVQFKNGDGQPKAVRVPGHED GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHP LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG QRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLLGELTVTG SSPDSLSLSWTVPQQRFDSFTVQYKDRDGRPQVVRVGGEESEVT VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQQRFDSFT VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWTRQPGFGCKAVRCASGRCTVRDFIHRHCQDQN VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGPGSML RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK GMQAASSKMVSABISENRKRQWPTKSQTDRGASAGKRRCPWLGM EGLETAEGSNSESSSDDDSSEAPSTSGMGFHAPKIGSNGVEMAAK PPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETETQEKKAESKEPIEEEPTQAGLNKDKETEERT DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV AELELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGQTPLHSQGGGGGSGGGRRRTPRGMPKEKVEPPDPRRNVTI MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	3	429	LDKDTGLIMLYARLDYELIQRFTLTIIARDGGGEETTGRVRINV LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDPVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL
5765	3	825	QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTG AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGPGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEECSHRRIKKLKTEKVDPLF TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLYLALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPGLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVRLVGVTVPPSFLV FGMYGR
5767	2	892	NFRATPRPPTPRPELRTGTEVILWYLDWRALMKRKMKANIKLVG SGFPLPSSDLDDSLTEEIDSKIGFRNDANFDWQNVADFRDAGGS LTEVKVEEEERDPQSPEPEIEEEEEMLGSVIPDSRRENELPDFP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			HIDEFPTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIERERKLRLQIV NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ FLKFPESEKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL SRVTSLANLPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRVDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQFAMLLRE YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRDPIPDQDIGVPEGP LEGVGIREGGILTDSPGRIKRSMSSTSASAVRSYDGAAQRPEAQ AFHRLLADITHDIE
5772	148	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG ILTFSNLVTCSAIYHLPVFPERSPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPPSSSSG RRLNISYTRNMTLKDGKNSK
5774	2	592	FVEEENIRVVRCGGSELNFRRAVPSADSKYIFCVSGDFVKVVST VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI DGILIKTFIVGCKLHALPTLAQAEDSVFVIVNKEKPDIFQLVSV KLPKSSSQEVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLMKGWDRKAQRNGL RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLPVPPDIDRRTVELRIGGNF IIHISRQDFANMTGLVDLTLSRNTISHIQPPSPLDLESLRSLHL DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL EDLDLSYNNLHGPAVGLRGDANVQPSTS
5777	2	949	GQDPEPGQDLFQPERKVDPSWGRGREPRLGKLRPQNDHLSVLKQ VKKLEQALKDISAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV
5778	1	1210	QRRQSVSRLLLDVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LPLPTEKFLQELHQYFVRAGGNEGPEGLGRKQACLAMLLHFLDT YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLPEEIQVSPGDTEYHRVEPEDVANHLTAFHWELPRCVHELEPV DYVPHGE
5779	138	1671	EAVQVLIKHSADVNARDKNWQTPLIVAAANKAVKCAEVIIPLLS SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI KLLQSSGADFHKKDKCGRTPLHYAAANCHPHCIETLVTTGANVN ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QFPRVITCLPFKGPDVRLYKSEPELTTVAEVDESNGEEKSEPVS EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHQQACLREK KKQLNVIGASDQSPLQSPSNLRDNP
5781	19	941	RGSLGGHPWREPMRAASQGCLPVSPVTGPHQERAVGGRGPGGAP PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ VQPHPTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT QHSIHTVTCKSPRQKEDRSPXPPQAPKHPEEHGRQS\QAPPPLP VAPSRTCGGC*TWDPALLVS?/PQGDSTPELPAP\QQPTGGPSR CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAVNVPSLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP PEPESSITLTPVESAVVAEEHEVVPERPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNIMNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPPALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNSPLPVKRD\DQ TLAALI\SLXESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSRHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSRS/RDRRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRGSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEEEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEPPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVPSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y
5783	1693	698	DSGLRVAFTMEGISNPKTPSKLSEKKKSVLCSTPTINIFASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRGVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL NDLIEE/PI*SQ/PKILFQQP/LILKVALNNMARGLKYLHQEKKL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENNTVTDPEACYI GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLS NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIE LFSVCTNEDPKDRPSAAHIVEALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQNDHVHL ODNYNLGSFTPQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQNDHVHL QDNYNLGSFTPQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5786	1532	1674	SYKLPAAERRASSCSQPPTPTRRRNFAPGRTSRGHRPQM*SGTP APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRFPRNWNPMMAE
5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARELLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFINAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS
5788	2	6860	EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNBRSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLME:LKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGCATTQSKSSTKKSKKEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS TETLQCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LCNACGFCKYARFDPMLYAKPCCAVDPIENEEDRKKAVSNINTL LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPQDDSGTAGGIS STSASVNRYILQLAQEYCGDCKNSFDELSKIIQKVFASRKELLE YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA AAMREEVRQLMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIKTP VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVEALTTVKPYCN EIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT QAARQNACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA TLSTDLQQGYALKSLTGLLSSPVEVESIKRHFKSRLVGTVLNGY LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI ETAKRYNLDDYRTPVFIFERLCSIIYPEENEVTEFFVTLEKDPQ QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG LLGDATEEFIESLDSTTDEEEDEEEVYKMAGVMAQCGGLECMLN RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIIP YLSPGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK IAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/BAA RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI PNLHKLEQVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR RETRAEKKRMAMAMRQKALGTLG\MTTNEKGQVVD/TRTALLEA DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW ENKPRETSRATSTVSHFNIVGYDC\HLA\AVSLARGREEWESAA LQNANTKCNGLLPVWGPHVPESAPATCLARHNTYLQECTGQREP TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR HNDMPIYEAADKALKTFQEEFMPVETPSEFLDVAGLLSEITDPS SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ TEEKEKKEKPKSDKTEEIAEEEETVFPKAKQVKKKAEPSEVDMN GPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP EPDCNPSEAASEESNSEIEQEIPVEQKEG\APSNFPISEETIKL LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQRQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQNKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGPVTM ILQCSIEMPNISVAWKELKEQLGEEIDSKVKGMVPLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ
5790	3786	1585	ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEEESESESDSDSDGGEEE DAEEEEEEKEENEGHKWSTGEEYIAVGDPTAQQVGDLTFKKGSI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN HVSFCYLIVLMRNRMETVEDTNGSETGFRAWNVQSRGRIPLVSK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLEEGNQFRANYFLQ PELMPSQLAFRDLMWDATEGTIRSRPSRISLILTLWSCKMIPLP GMSIQVLSRHVRLCLPDGNKVLSNIHTVRATWQPKKPKTWTPSP QVTRILPCLLDGDCFIRSNSASPDLGILFELGISYIRNSTGERG ELSCGWVFLKLFDASGVPIPAKTYELFLNGGTPYEKGIEVDPSI SRRAHGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPML LEQPDVMDALRSSWAGQES\TLKRSEKR\PKEFLKVPRFLLVYH \GCVLPLL/HTPTRLPPFRWAEEETETARWKVITDFLKQNQENQ GALQALLSPDGVHEPFDLSEQTYDFLGEMRKNAV
5791	1	1636	LRVAEFAGTSR/YGAGLIQPLHRAPARDHGLLRGGAAPALSVSH GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLPDQLV NRSIQQGFCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQPIVDY IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLYFISPTGHSLKTL DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSNG VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGNKMVKA RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREQTHTRHYEL YRRCKLEENGFTDVGPENKPVSVQETYEAKRIIEFHGERQRKEEE MKQMFVQRVKEKEAILKEAERELQAKFEHLKRLHQEERMKLEEK RRLLEEEIIAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ LLIFMEKYFQVQGQYISQSE
5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVVTRFCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE ZKATRAPHTD
5793	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVNYGIVYTRFCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGRSDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD
5794	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAGVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GEPGEFYFDLRLKGDKGDPGPPGQPGMPGRAGSPGRDGHPGLPG PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG DKGQAGFPGGPGSPGLPGPKGEPGKIVPLPGPPGAEGLPGSPGF PGPQGDRGPPGTPGR\PGL\PGEKGAVG\QPGIGFPGPPGPKGV DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG SKGENGVWGTPGQPGSPGPWGAPGLPGEKGD\HGFPGSSGPRGD PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP GPKGSVGGMGLPGTPGEKGVPGIPGPQGSPGLPGDKGAKGEKGQ AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGRAGIPG TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGLPGRGFPGPPGAKG DKGSKGEVGFPGLAGSPGIPGSKGEQGFMGPPGPQGQPGLPGSP GHATEGPKGDRGPQGQPGLPGLPGPKGPPGLPGIDGVKGDKGNP GWPGAPGVPGPKGDPGFQGMPGIGGSPGITGSKGDMGPPGVPGF QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGPYDIIKGEP GLPGPEGPPGLKGLQGLPGPKGQGGVTGLVGIPGPPGIPGFDGA PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL VTRHSQTIDDPQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG SCLRKFSTMPFLYCNINNVCNFASRNDYSYWLSTPEPMPMSMAP ITGENIRPFISRCAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWI GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPPIECHGRGTCN YYANAYSFWLATIERSEMPKKPTPSTLKAGELRTHVSRCQVCMR RT
5795	1192	61	STRSPTVEYISAHPHILFMLLKGVEAPQIALRCGIMLRECTRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTRRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVELLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR
5796	2	1078	GRVGWELWCWYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQQPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG
5797	2	891	PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVSSSQEANAEVMRENTKKLVSQVEEKLQEEQR KHSARKEALLEETNSFLKAIEEANKKMQAARISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISPLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
5798	644	115	KILGSRWKSNSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFPTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
5799	2679	1435	LLSTYIKPINLFPETKATYQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPPFERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADBLLNKPVCKNNGVLPENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFPQPTEM AAQDFFQRWKQLSLPQQBAQKIFKANHPMDAEVTKAKLLGFGSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLPPETKATIQGVLRAGSQLRNADVELQQRAVEVL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM AAQDPFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL RTSKEPVSRHLCELLAQQF
5801	3	1413	FFRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLLNVDGVELT EVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG GYEEYNGNKPPFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV ITQRLTR
5803	2234	1299	EAQPGTTAEIYAYREEQDFGIEIVKVKAIGRQRFKVLELRTQSD GIQQAKVQILPECVLPSTMSAVQLESLNKCQIPPSKPVSREDQC SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE WDENLKDDSLPSNPIDPSYRVAACLPIDDVLRIQLLKIGSAIQR LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN PHGYVHETLTVYKACNLNLIGRPSTEHSWPPGYAWTVAQCKICA SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI LCL
5804	2	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKIQRELAKRAEQIE DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE REEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESSEAKK ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAPEE ARRQMVNEDEENQDTAKIFKGYRPGKLKLSFEEMERQRREDEKR KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP GKLEINFEELLKQKMEEEKRRTEEERKHKLEMEKQEFEQLRQEM GEEEEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGQLS EKEIQKKIEEERARRRAIDLEIKEREAENFHEEDDVDVRPARKS EAPFTHKVNMKARFEQMAKAREEEEQRRIEEQKLLRMQPEQREI DAALQKKREEEEEEEGSIMNGSTARDEEQTRSGAPWFKKPLKNT SVVDSEPVRPTVKVTGEPKPEITWFEGEILQDGEDYQYIERGE TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS APKESQQQSEDREYEVKERLYPKSKRRYDTYNIAGYQGSEIEVGL YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTR RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSEPLQVERCRRNLV ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRPLGFAVPLLPW ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RPSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMMLLRPLLVKKIACGLGKSDRPKSIYAALYFFPILTVLQAVGG GLLYYAFPYIILVLSLVTLAVYMSASEIENCYDLLVRKKRLIVL FSHWLLHAVGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNFKDFGELRYNECLMNFSCNGKNGSS EGRITHGFQLKSAYEHNLMPYTNYTFDFKGVIDYIFYSKTHMNV IGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP LVNGVHLPNRR
5809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADYDECEVSGLCRHGG RCVNTHGSFECYCMDGYLPRNGPEPPHPTTDATSCTEIDCGTPP EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI SIFNETCLKLNRRSRKVGSEHMYQPTVLGQRNYLANFSHATSFN PTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRNYQKEF AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSELPVVISL TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHISCAV WAQVKDSSLMLLQMAGVGLGSLAVVIILTPLSFSAV
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLHIEAFVS EIESPFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAQSFEE VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDQMLK QVAVPQQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME EPQDDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATRWRPTTPEA TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFPYV RAINAFGTSEQSEAALISTRTRFLLLRETAHPALHIESSGTVI SFGERRRLTEIPSVLGEELPSCGQHYNETTVTDCPAYRLGICSS SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG KCTLHLGIEPPDSVRHK
5811	1918	851	AAALADPLPEDKWSAEKRRPLKSSLGYEITPSLLNPDPKSHDVY WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNPLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEQLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQENVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD
5812	5204	2744	GGRQRCQRGRSCGARERREVEPGTARPPPAASAMDASLEKYADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEEKRE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAPLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTGNKPTDKLRALPLNLSLQYLGLDGPVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPQSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS EERLLEEGVLRQIPVVGSVLNWPSPVQALQKQRTFNLTAGSLEG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TEPIYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL PRNVMFVPFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL GQVALRTSLELNMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY QSIYDTAENINVSYPEWLEPLKR/ETWNFG*QDTAKALADVATV LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS ILQGRDLRSYLG*RGLPQH\YIAV\SSPTNTIYV/VLQYALANL TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFL IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA VSY
5814	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTNMGSEDHLGVIPQ GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE TKMNQRSSRSHTIFRMILESRSKGEPSNCEGSVKVSHLNLVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQQEL KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK KDQENQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENSALREEVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQSEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK IQELKANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSK LEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDQLK ESLQETKARDLEIQQELKTARMLSKEEKETVDKLREKISEKTIQ ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE LRRIKESLKMERDQFIATLRENIARDRQNHQVKPEKRLLSDGQQ HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH RIMKKLKYVLSYVTKIKEECHECINKFEMDFIDEVEKQKELLIK IQHLQQDCDVPSRELRDLKLNQNMDLHIEEILKDFSESEPPSIK TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV NNFFNNRIEAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRELE NSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKC LEKTKETIQVLQDKVAIGAKPYKEEIEDLKMKLGKIDLEKMKNA KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK DVP\ECKTQ
5815	23	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET VDRLLKGYDIRLRPDPGGPPVDVGMRIDVASIDMVSEVNMDYTL TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\ QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAFGAQPSPP TVYHERQRLELCAVHALNNVLQQQLFSQEAADEICKRLAPDSRL NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ VLGLILNLPSPVSLGLLSLPLRRRHLRNPCARL/VTVSYYNLDS K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG SWLRTD
5817	851	118	RLPRGPGANRGRSCRGCSGGREPSGGALPKRHCDC*PPSPPAAD VMSNTTVPNAPQANSDSMVGYVLGPPFLITLVGVVVAVVMYVQK XKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCIGPCHLLPLLSP GSPCMVLGLHPSLHPPSAASASHALTITSLPPGLLPFVGVELTA HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLNSTDDQQKIQAAAPDKGD DRRLGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK PLKKATGKDSPCLSIAGPSSSRSTDSSMEFSISTECLDEPKENGS TEEEKPSGHKLSFCDSPGQMNKNSVDSVKNSTVAIKSRPVSRVT NGTSNKKSIHECDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH DVRDNNNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK MKXQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ GIINLAFEDATENBCREFSANKKFKRSVLLSVDECEELGSDEGE VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLLGALHLVWTLVVAAARAEKEAFVQSESIIEVLRFDDGGL LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP KMEKVYLHNPSSE*TITLVSIPATTSHFHASFFQNRKILPGGNT SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN NILLITNASKPHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM WDADWDLHQSLFKGWTGIKENSGHRLGAIPEVNTDLQKNIISKI TABLSWPSILSSPRHLKFPLTNTNCSS\SEEITLENP/SQDVPV YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN SAHPLQSSTGFMEG\LSPHLILNLILKPGERKSVKVK\FTPVHN RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE ISGYSCEGYGFKVVNCQEFTLSANASRDIIILPTPDFTASRVIR ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH SSEDSDITSLIEAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG KPLQRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAPGNSFNLTGE VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPAS SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR RSSDPWSNSHPPHEN
5820	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEPEEKMN ENWKKELEKHRSKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\ SSSSDSSSSSSDSEDEDKKQGKRRKKKNRSHKSGSESSMSETES

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS ESEYIEEVRAKKKKSSEEREKATEKTKKKKKHKHSKKKKKAA SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF GIIPGLFSSHSDATV
5821	179	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN TYVIKLFDRSVDLAQPSENTPLYPICRAWMRNSPSVRERECSPS SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\ SRIPSPLAALRMQGTP*RWSPPEPEPSPSTLIYRNMQRWKRIRQ RWKEASHRNQLRYSESMKILREMYERQ
5822	464	4379	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA HGPHEVHPSSTDYNLMWTGSHLKPFLLRTLSBAQKVNHPPRSYE LTRKDRLYKNI:RMQHTHGFKAFHILPQTFLLPAEYAEPCNSYS KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY LKQEGRDTTALMAHVEDLIIXTIISAELAIATACKTFVPHRSSC FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD MFTVVGPVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA SDAEMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLPQDRMTADG APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP XYPVITQPAEMNVKTETESEEEEEVALDNEDEEQEASQEESAGF LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM ENPQEFIRQASEAELEEVLTFYTQKNKSASVPLGTHSKISKNNN NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP RCRSGSHTIGPPSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS GIAKTQKEGEDASLYSKRYNQSMVTAELQRLAEKQAARQYSPSS HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH KYHPTAGSYQLQPALQQLEQQKLQSRQLLDQSRARHQAIPGSQT LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP EDPRSQGVERPIQESK?\KINLFEKEKEMKKSPTSLKRETYYLS DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHGAHALP RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAQSHLGQGK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK ENVDSPLLKF
5824	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETVYLS DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP RRSCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATEVARREAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLFDICDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK ENVDSPLLKF
5825	2	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSHLSAPGMLHL SAAPPAPPPEVTATARPCLCSVGRRGCGGKMAAAGALERSFVEL SGAERERPRHPREFTVCSIGTANAVAGAVKYSESAGGFYYVESG KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFQNCS VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMYRSELVVD SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT GWMPTAIRGDQSPSDRPLSLAVHCVEHDAPIPALCQDHKLRMWS YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDP ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL DLSWSELKKEVTLAVENELQ3SVTEYEFSQEEFRNLQQEFWCKF YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD HLYLLPYENLLTEDSTTISDDVDIARDVICLIKCLRLIEESVTV DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLQ EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG TGQLFQAQQDLLHRTAPLLL3YYLIKNGSECLATDVPLDTLESN LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL FSQPKAPLSQTGLNWPEMITAITSYLLQLLMPSNPGCLFLECLM GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD VIGLPELVIQLATSAITBASDDW\KSQATL\RTCIFKHHL\DLG \HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG TVMFBYGMRLGREVRTLRGLEKQQNCYLAALNCLRLIRPEYAWI VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE CSLARIRLTLAQHDPSAVAVAGSSSAEEMVTLLVQAGLFDTAIS LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQAEAWAWLAANQLS SVITTKESSATDEANRLLSTYLERYKVQNNLYHHCVINKLLSHG VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC	
5826	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPCGQHG CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA PPQPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALXSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP EEMSPEPTTLPECHGHARDAPSFGTLVESLLTILNEQVSADVLS SFQQTLHSTLLNPIPKNRPALCTLLSHDFFRNDFLEVVNFLKSL TLKSEEEKTEFFKPLLDRVSCLSEELIASRLVPLLLNQLVPAEP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLV EVHEEHVRMVLLSHIEAYVGALSLREQLKKV\IL\PQVLLG\LR D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SP TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK SEEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN W
5828	2	257	AREGGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV MAVGGGSRMTDLTSSIPKPLLPVGNKFLIWYPLNLLERVGFEEV IVVTTRDVQKALCABPKMKMKPDIVCIPDDADMGTADSLRYIYP KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI EPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS EL\IPYLV/RGKQFSSASSCQGTRKEKEGGSKGKRGLKSFRISY SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGPANFVDFNPS GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY PRTPHPHEEKVETVEDFFLHLLRLIQSLK*SICRSLLPLLWISF LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR LTLTEDKLKDCLENQQKLPSAVQQKS
5830	4496	3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNW NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR PQPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELRFL LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLPWACSTNKPE GYRVSQALRENTYPPLAMIMLKDRRE*PV\VGRLZGLI\QPDDL INQLTFIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLASLR ADQEKERKKREERERKRRKKEEVQQQKLABERRRQNLQEEKERK LECLPPEPSPDDPESVKIIFKLPNDSRVERRPHFSQSLTVIHDF LFSLKESP\EKFQIBA\NFPRR\VLPCIPSEE\W2NPPTLQB\A GLSHTEVLFVQDLTDB
5831	71	2897	FCSKDKCCLYLPDSINKSKSCTAKPKAHSQDRHAVMDSERQVKD TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSPDSLDS FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAERREYR KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCEB EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE RSHSTEPNLSSPLNDPNPMKYLRQQSLPPPKPTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMPEGVARVH GSPLSLKQDNGSIEINIKKPNSVPQELAATTGKTEPNSQEDKND GGKSRKGNIELASSEPQHPTTTVTRCSPTVAPVEPPSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPPFLD KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEERRR QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEERRY YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEGAL AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL
5832	2454	829	PGRRFRHGSCAFQKQCYMLHICQVPLQGECKFGTSCKRSHDPSN SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R PGSHLEVPQRKAQLRVRPQSLRSEKPGLWHN*KGLPQTQIR\AP QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE YQKVNNLFNRTLPFYFVQKIERVQNLALWEVYQNQKGQMQKQNG GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF RNRELEATRRQRMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN EMYGTPSVPLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII GGSRYVAGIEGPFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDEIL KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH SALIYFLGTPLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGAPPASPSDSLGQQNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTINFEDR NAPVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKPINMPAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYYENRMYLTPSEKHMLLKVMGP GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYHVRTMLESLIADKSGSK XTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDBIEAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LIERLGTPQQIAIAREGDLLTKERLCCGLSMPEVILTRIRSFLD DPIWRGPLPSNGVMHVDECVEPHRLWSAMQFVYCIPVGTHEFTV EQCPGDGLHWAGCMIIVLLGQQRRPAVLDFCYHLLKVQKIDGKD EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLQ SQNIYHHGREQSRMNGSRTLTHSISDGQLQGGQSNSELPQQEPQ TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT PRFNPIMVTLAPNIQTGRNTPTSLHIIHQVPPPVLNSPQQNSIYI RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVVQPSQPGPWTTC PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSQS SQSSAHSQYNIQNISTGPRKNQIEIKLEPPQRNNSSKLRSSGPR TSSTSSSVNSQTLNRMQPTVYIAASPPNTDELMSRSQPKVYISA NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ KARMERLQRELEIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA CTFLNHPALIRCEQCEMPRHP
5836	361	2303	FHITWCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVPLMNGEIFSGIK VEAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA* VKPQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE PIDLLNVAPIAEEKTMPTTFWREGNKQKNKCEIPSEEFSKDVAA AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME ELQKLRRTRICILIRPLDTVLDDDIGCAVWFASRQIGWLVAQEG VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM MELGRISSRNLGRDDRVIGDHGKEARFPPFLDENVVSFLNSLPIW EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA KMEKINEKASDKCGRLQIMSLENLSIEIEKETKL
5837	4792	903	NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL KRRGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT QSWRRKYTLFSASSEGQNHSRIVPNLCPLQTEDDKQLLLSTSMD RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL VFCPPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVANSPL DPDCIYSG\ADDPCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ EGEEQARERELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA GYHVWLWAVEAPAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA LRCAQELLLANNWVGAQEALQLHESLQGQRLVPCLLELLSRHLE EKQLSEGKSSSSYHTWNTGTEGPPVERVTAVWKSIPSLDTPEQY QEAPQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DEAVQALLRAVVRSYDSGSPTIMQEVYSAFLPDGCDHLRDKLGDHQSPATPAFKSLEAFFLYGRLYEFWNSLSRPCPNSSVWVRAGHRTLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERMLSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKSTANGPDKNSPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTEANQRMAKFPPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQQAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDPSQEEWECLDPAQRDLYRDVMLENYSNLISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNGLGDNMECKGNLEGQVSKSEGLYMCVKITCEEKATESHSTSSTFHRII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKHRNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQKIHTNEKPYQCNACGKAFIRGSQLTEHQRVHTGEKPYDCKKCGKAFSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSGEKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCASQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPYKCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLSEHQRIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKECGKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQRIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKECGRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRLHN*EYSSHKICMHSIALASLDFAHLQEKNPEN
5839	1	2425	GRPFPRPPRALPRLPLRGRRQDGRWTVDPEECLKD\SPRFRAALEEVEGDVAELELKL\DKLVKLCIA\MIDTGKAPCVANKQFMNGIRD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNSEIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPVPSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSEILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDAAKEKREMECKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFKRASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVKHCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\ATAYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQCIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSKVRSLTLDTWEPELLKLMCELGNDVINRVYEAMVEKMGIKKPQPGQRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSSEEKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRRSLPSTVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKMAEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGANVNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEEGKDPLSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIFRDFSQMASNNPEKLNRPQQDSQKF
5840	698	3610	KHLHLPRQHLTTLWQISSPRWRSPQRA?MSALSKTQTQSAPALQGLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSSAQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLPSNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQRGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLLSKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPPGLGSESPYKQPSDGMERPSSLMDSSQEKFYPDTSFQSDEDYRDFEYSGPPPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGVKSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSPSPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRSLFSPQNTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNASRKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQEEHYRIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQTVESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELASLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHHLPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIVSRDAPTHLPSVDLSNPPTKEAALAHAAPPPPPGEHSGIPPPTPPPPPPPPGEHSSSGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVPPKDHSSLLQGTLAEHPGVLPGPRDHGGPTQRDLNGPGLSRVRESL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSGII LRSPRPDFRPREPPLSRDPPHSLKRPRPPPFARGPPPFAPKRPFFPPRY
5841	1908	762	GLRLPLVLTVWPMMKPSWLSRTEPSKRLLCRTLWCQSGWSSRSYTRSMLKMTTSINRRSRTSTKSTRTSARPGLTA1VSIGLSDSPTWRHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSPPGDGLDSGLARRGSAVSALASGLVEEPMLGPPPHPTPRPKAVSAKSKEDLVSQGFTEFTIEDFIINTFMDLIEQVEKQTSVADLLASFNDQSTSDYLVVYLRLLTSGYLQRESKPFEHFIEGGRTVKEFCQ\QS\VEPMCKESDHIHIIALAQGLQRVHPGWEYMGPRPRAATTNPHIPP*GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARALGHCYRGPSVVVKWSYFTPFFLSHDPPPMFY
5842	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKLWSSRRPRTRRNLLLGTACAIYLGPLVSQVGRASLQHGQAAEKGPHRSRDTAEPSFPEIPLDGTLAPPESQGNGSTLQPNVVYITLRSKRSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPQEA\EGKLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLQPSSRESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGARLLLVLEGGAPGAVLRCGPSPSPCGLLKQPLDMSEVFAFHLDRILGLNRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTWGTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQIYNRLDTNCCGFRPRKEDACVQNGLRPKCDDQQSAALAHIIQRKHDPHHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQHLRQKLLQSLPLDKGYWESQGGRQGIEKLIDVIEHRAKILITYINAHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGMRGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTPMIPGEKVAHTSLDALVTFHQQKPIEPRRELLTQPCRQKDPANVDYEDLFLYSNAVAEEAACPVSAPEEASPKPVLCHQSKERKPSAEN/RQNNHQGSHPLLPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVTLGCPEIHGDLRPWDRKRQPRSLRGGSHLGGGRLHGSLCGHISQKPLTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPGVQARAPGLGRA
5844	202	2471	FDSAVLSSINVNAVLPGPLQLLGVLLTYSLSSIRLIQAAYAYGIKPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHLQYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQGPRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGMPGKPGAMGMPGAKGEIJQKGEIGPMGIP*PQGPPGPHGLPGIGKPGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGVKGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEPGPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGLPGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGAPGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIGVGPGGPGPKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHQQKGVPGLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYGAKKGKNGGPAYEMPAPTAELTAPFPPVQAPVKFNKLLYNGRQNYNPQTGIPTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHSSFSGYLLYPM
5845	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNERGPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLPKPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPKPPPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKTRQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKSEISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAEGEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HPPKKRPKTIVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRREFVMQVKVGNEVATGTGPNKKIAKKNAAEANLLQLGYKASTNLQDQLEKTGENKGWSGPKPGFPEPTNNTPKGILHLGPDVYQEMEAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion; \=possible nucleotide insertion)
			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG N.
5846	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK LQGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKEIKVTEKTIPS WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK KEKSCKCNECGKAFSYCSALIRHQRTHTGEKPYKCN*/CVEKAP SRSENLINHQRIHTGDKPYKCDQCGKGFIGPSLTQHQRIHTGE KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTQHQKIHTGEKTYK CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSQHSNLTQ HQKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF SYGSSLIQHRRIHTGERPYKCNECGRAFNQNIHLTQHKRIHTGA KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRVTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTEIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHISKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIPYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF
5849	3545	1895	KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLPGPLTRPPHNMMKDFILTVSI VICVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE CELSRRQYAEQELEQVRMALKKAEKEFELRSSWSVPDALQKWLQ LTHEVEVQYYNIKRQNAEMQLAIAKDEAEKIKKRSTVPGTLHV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGPQ IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNEEE EEAIYPSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN IIS/DERYQEMRCP*RIPSGGIL
5850	3	1895	KAVLNPSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN LICRQKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVPCE SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG DTGSAVLNGPSRLNKNDKQRIAVVAFPPENGVSDPQKAQIIGSQ RENGWAVGVESDFDFCQTAIKRIFNDSDPTGFLTVEYGTILSSA NSINWGRLLPQVVYHASAYLDLVSQGGFISFGSPVDVCIPTGNPG NILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKE N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD PHTAVAKVVADRVQDKTCPVIISSTAHYSKPAPAIMQALKIKBI NETSSSQLYLLGSYNALPPLHEALLERTKQQSKMEYQVCAADMN VLKSHVEQLVQNQFI
5851	3120	1802	RCYLQFLALLLTSTSARAAAATAAAEEPAGSPSVWTRAGDHNRQ RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHPAVSVFLVELY GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI LAPMAVCQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT PALAVKAGLKEEETELKQLNLHKDTEPXPLEQTHLMGVKDSNIH ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY LATSKMWPGSDRSDLRIGTAFLFDIVCDLCIHAWKPPGLVRFSF
5852	1	422	KITFPSSLCPLRQLPEVRGYSGQPLTDPLYISLCRSHKCRGKGWG SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGPPITGGPG/WPRQ YYFFISGRH*VLFTESDPYYVAMDPGGHGLSSHYSPGVPYYLQT FVSEIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLLGLSRVKGLHGPAASAWIEDPETKGDPGGPWGMWRGSDLRPR PVSLTGLTLVCK*AAQGPQV\HSVKLCPGLGG\PCLL\PPIFRP LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESB SRWVRGNFRTGTAATLIGPSRNPTLNGSENWGSLVSIQEEGPDT GWERSKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE LKHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS GAETIKDLLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH IRVTFL/KFQRRNILQASSQRKQVTYKQAKVRLTSDFSPAILNA RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKQNWKTFLDIQG LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSYGCKAPSRISHLHK\FLPLLLPSLLWGYSESPPPITDSWAP FISLTHHVLSQSQSPLSSNCWICLSTHTQ*PTALPADLLTWTQS NVSLHISYLAIPPLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS GRAVALLHLIASQLTSIQTNTASSKPPIWGY\LSTQTSPISPPP LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/KTPCRPSILHPNY KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL PTFTYNPCLSTPSLPFLCDTN*YLCLPANWSGTCTLVPQAPTIN ILPPNQTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT GIAGITTSITSYQTLPTTLSNTVEDMHTSITSLQRQLDFLVGVI LQNWRVLDLLTTEKGGTCIYLQEECCPCVNESGIVHIAVRRLHD RAAEL*HQVADSMWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTPHLYGGIILLLLIPISIAGILYK FQDVLLYFPEQPSSSRLYVFMPTGIPHENIFIRTKDGIRLNLIL IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLPSFPP MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ LYELSPSRTKRLAIPPDGTHNDTWQCQGYFTALEQFIKEVVKSH SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAPAVEPQGPALGSEPMMLGSPTSPKPG VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS* NMWMSNTGNWMHIRYQSKLQARKALSKDGRIPGESIMIGVKPCI DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMPGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAP PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP PSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGPGPGGGKMP GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC LLGIYLLISRRMNSRRLFAKIWENQEKPLSTKAKDSEPIKLESR ALA*NCPKFELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN PAS
5859	307	1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL RTPIQRTPHEINRRESNRLSAPSYLARSLADVPREYGSSQSFVT EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS VDWTMRGRKYYIDHNTNTTHWSHPLSREGLPPGWERVESSEFGT YYVDHTNKKAQY\RHPCAPTCTSV*ST*SCHI/AS/RQQTERNQ SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT YQQMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ HGKNP
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATI TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF CYRRRRTPRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL KMGMKFVSDEHYDENEDDLVSHVDGSVISRRENYV
5861	2051	1305	EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL SEGEQGIPTACAAPAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI LE*RMNSGSPARDNAPSQRPCTNLSEGLRFGISPSWREALYGCH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			A
5862	1556	483	PPPQLIMGEIKVSPDVNWFRGTVPLKKIIVDDDDSKIWSLYDAG PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYM DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS GPVDPMMADAIDFMVDRLESLGQSELASRLTLNCQNSYVEPHKI RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQMSVPRSLRCRKA ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPFPSGSSGS PVLTVSGK
5863	2714	249	PFPSRGSLFLAAPREDTNGPLMVLFCLLFLYPGLADSAPSCPQN VNISGGTPTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVQGNVSF ECEDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL GP\VRTGPRFGHGDKVRYRCSGNLVLTGSSERECQGNGVMSGTE PICRQPYSYDFPEDVAPALGTSFSHMLGATNPTQKTKESLGRKI QIQRSGHLNLYLLLDCSQSVSENDFLIFKESASLMVDRIFSFSI NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKDHEN GTGTNTYAALNSVYLMMNNQMRLLGNETMAW\QEIRHAIILL\T DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV DWRELNELGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT AAHCFRDGNDHSLNRVNVGDPKSQWGKEPLIIGKAVISPGFDVFA KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \EANLGFLRETFKGSTCR\DHENEL/VNNKQSV\PAHF\VAL\N GSKLEHILTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRR\VVT D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS EWATLRTL
5864	173	1013	PLYSVPQSLISLPQPLLCPPGGQEPSAPSPCLYSPLWACSFTWG KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQPHSVTSPPPPAQQPTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP
5865	568	1684	CLPGPRWGEGWRAGHTIVGCTFFKTAI*SHPKGGNVLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACSCLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCPSIKPELKAKKKK
5866	98	3197	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVANTEHKMSVEEVCRKYNTDCVQGLTHSKAQSILARDGPNA LTPPPTTPEWVKPCRQLPGGPSILLWIGAILCFLAVGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLRAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIDPPRAAVPDAVG KCRSAGIKVIMVTGDHPITAKAIAKGVGIIPEGNETVEDIAARL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NIPVSQVNPRDAKACVIHGTDLKDPTSEQIDEILQNHTEIVPAR TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI AGSDVSKQAADMILLDDNFASIVTGVEEGRLIFDNLKKSIAYTL TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE DFSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAPG GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA PDHCSDDA*QSCPAAAAAAPLQRQCDQSQGQITSPQSGNSGSTFS ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5870	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSWRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHEIL QKLNDCSCLASQAILLGILLKREGPNPITKEGTVSDHIERVYRR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAVC HEEEVISNPLSPRVIQNIIYYKCNTHDERE AVIQQELVIHIGWI ISNNPELFSGTLKIRIGNIIHAMEYELQIRGGDKPALDLYQLSP SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI LERTPNGIIVAGKHLPQQPTLSDMTMYEMNPSLLVEDTLGNIDQ PQYRQIVVELLMVVSIVLERNPELEPQDKVDLDRLVKEAFNEPQ KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG EVKPNNDDPCLIS
5872	68	665	VQQYMYRFVIKINSCYSEKTSICHRRCCPELPATQPWPTPTVPF NIAIDSESLGCI\SFKLFADKV/PKRWKKNPVLLNTGEKVLQDK GPCPYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENFI/LKH TAPGVLSTANAGPTTKGSQFFICTAKTEDG*QHVVPGKVKDGMS IVEALERSGSRNGKTSKKITAANCGQL
5873	2240	506	RRPPEGGSGGGRRTRARMPLPWSLALPLLLSWVAGGFGNAASAR HHGLLASARQPGVCHYGTKLACCYGWRRNSKQVCEATCEPGCKP GECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGS YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTPGSYYCKCH IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKC KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFPPKVNEAGE FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\ EDDFDW\NPADR\DNAI\GFV\MAVPGLWQGHK\KDIGRLKLLL PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTGE DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS GLCPDSLLSVDD
5874	2	3387	ACPRLARRRRRVRSLRRRRGWLRARWSRGQNNMAARRYTQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKPALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLRKS\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRPGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMKLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKAEPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEQSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLNPL\HDQNSG\APK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLMB GEAEPEDEPPPREAELESPEVMPEEEDEDDEDGGHEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALPTGLLQVTCFPPG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IPVF
5875	296	1848	LAALGGLPLWRLSRRGPREVLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLPPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGNFHLFDLTPAR VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKNMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS /SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESSGS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	)		GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG NGHEEVVACAWDGQTYIIDHNRTVVRFQVDENIRAFCAGLYACK EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKQ
5876	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAAWLKKIFGDHPIPQYEV NPRTTEILHHLSERNRVRDRDVYLVIEDLKQKASEYESEAKYLQ DLLMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP AVNDLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEPRFGIQAAGEQL SARGQ\DAPSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD LMP\NPSHCSK*RIEBAK\RELA\SIEAELTRRVS\MMEL
5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV LSRELIEMLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR CPCSTVS/NGSQMTCR*INIILILQKSVCEL
5878	950	2113	GLWKCMQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY RMLRSLLSAQGVSPQMITVFIDGYYEEPNDVVALFGLRGIQHTP ISIKNARVSQHYKASLTATFNLPPEAKFAVVLEEDLDIAVDFFS FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECII PDVSRSYHFGIVGLNMNGYFHRAYFKKHKFNTVPGVQLRNVDSL KKEAYEVEVHRLLSEAEVLDHSKNPCEDSPLPDTEGHTYVAFIR MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV GVPASPYSVKKPPSVTPIFLEPPPKEEJAPGAPEQT
5879	3	981	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTFALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT EITRYSFYTFSLLDHLPYPIKWARYNFFIILYPVGVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSFDYYYPLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIVWFLKI
5880	1138	1324	SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ
5881	26	441	GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV
5882	2407	2216	SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPIAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER NEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPPEALFRSQHYAL LDNSCREYLPICEPFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY LADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRVAEPSSALV SINQTIPNERTMQLLGQLQVEVENFVLRVAAEFSSRKEQLVPLI NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEPIEELLS PPFGGLVAFVKEAEALIBRGQAESRLRGEEARVTQLIRGPGSSWK SSVESLSQDVMRSFTNPRNGTSIIQGALTQLIQ\LYHRFHRV\L SQPQLRALPARAELININHHLMVELKKHKPNF
5883	2	1374	EFPGRRFRAVMEAGAGAGAGAAGWSCPGPGPTVTTLGSYEAAEG CERKKGQRWGSLERRGMQAMEGEVLLPALYEEEEEEEEEEEEEVE EEEEQVQKGGSVGSLSVNKIRGLSLTETELEELRAQVLQLVAEL EETRELAGQHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG ELRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEEYRALQESNS SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDPLEP DPEMQLLRQQLRDAEEQMHGMKNKCQELCCRLEELQHHRQVSEE EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL*A LVVISALLWCWWAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR SRLRDCGDYTPSERLGPKGAMLWFQQAIPAAIATAKRSGAVPVV FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQP SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVRQM HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE IPSTSDTKSDTTATGGESAGHATSSQEPSGCSDQRPAEDLNIRVE RLTKKLEERREEKRKEEEQREIKKEIERRKTGKEMLDYKRKQEE ELTKRMLERRNEKAEDRAARERIKQQIALDRAERAARFAKTKE EVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSF TNQFPSDAPLEZARQFAAQTVGNTYGNFSLATMFPRREFTKEDY KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSEPPNPAS SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNTW NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV IYWFRQIIAVVLGVIWGVLPLRGFLGIAGPCLINAGVLYLYFSN YLQIDEEEYCGTWELTKEGFMTSPA/IVHGHLDHLLHCHPL*LM VYSSQVLPIQSKGPS
5886	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS GTPGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG MPGLTAYPGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLEETLKKASPDGY DCYFDNVGGEFSNTVIGQMNKFGRIAICGAISTYNRTGPLPPGP PPBIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPQPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTAMPPQRVPELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY VSPTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAPYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYQQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHPITQSFNRK DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPFNFFPPF V

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQFSKRPRCDDSPRTPSNTPSAEADWSPG LELHPDYKTWGPEQVCSFLRRGGPEEPVLLKNIRENSITGALLP CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRPEH SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVMB QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT DAFLKADDYIEITGAGGKKYRISTAIDDMBAYTKLTDNIFLEIL YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS LYA\ARQYFVQN\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\ NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMNVPQR KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLPTYHLQRLL AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY AIPVALQKAGLTVSDVDIFEINE\AFASQAAAYCVEKLRLPP*EG *TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKATKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR TAVKWMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGHSQS QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYPGPCN SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALKDSSNFSVS FLLKILGLLAVVVAPF\CQLQWS
5894	174	1673	RYSPKKVLQNKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE DHYSTWEQGFKLQQNSKGLGQEPLCKQFRQLRYEETTGPREALS RLRELCQQWLQPETHTKEHILELLVLEQFLIILPKELQARVQDR HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKILVEEMAPL KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES SGKISEPMEAHNEGSNLERHQAKPKEKIEYKCSEREQRFIQHLD LIEHASTHTGKKLCESDVCQSSSLTGHKKVLS*ERKVIQC\HGV LGKAFQRSSHLVRHQKIHLGEKPYQCNECGKVFSQNAGLLEHLR IHTGEKPYLCIHCGKNFRRSSHLNRHQRIHSQEEPCECKECGKT FSQALLLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSECGEAFRQR SGLFQHQRYHHKDKLA
5895	2967	86	HPSLLGAIPFVPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLPVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYFL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAA3VAKLLDLKKQLAVAEG KPPEAPKGKKKK
5896	2967	86	HPSLLGAIPFVPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLPVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYFL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5897	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLPVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPPLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPPHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA PSWTDLLLKNNS\ELLNNLGNFINRA\GMPVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5898	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLPVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPPLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA PSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5899	326	1078	NCPKSKEPNGVRAPSLPSPLRAAAMALSDVDVKKQIKHMMAFIEQ EANEKAEEIDAKAEEEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALPGANTNRKFFI
5900	64	1409	KAAGRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA LDRHTDTTYFQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QKAPEEPELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG /YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE SCDKQFTSVDDLQKHLLDMHTPVFFRCTLCQEVFDSKVSIQLHL \AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVIIK CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL REKHCVPETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSII DGSGEDVDTSEPNYGCDICGAAYTMETLLQNHQLRDHNIRPGES AIVKKKAELIKGNYKCNVCSRTPFSENGLREHMCTHLGPVKHYM CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL KTRCS*LATPKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV PVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ HSS
5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLPTYLDHTADVQ*V*REP IPLKPRQ*ED*MFQSWLHAWGDTLEEAPEQCAMAMPGYMTDTGT VEPLQTVEVETQGDDLQSLLPHFLDEWLYKFSADEFFIP\GWGE EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGPTTGR\RGDL ATIHGMNRPPLLLMATPLERAQHLQS\SRHRQAL\DTNY\CPSF HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\IIB\PKGYHANPC\L GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW ALGNSETEKAFKAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ HEKWYQKFLALEERKKESIQIWKTKKQQKRESIFKLKSKADNTP VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKGIEMSMKCASQL KEEEEKEKKHQKERQRQFKLKLLLESYTQQKKEQEEFLRLEKSI REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAPAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAPGSSVPEKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIPQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILPRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*PGKNKMVKF*PIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLFISVYFS*LVFGINGFQYSPVVKLHCLYPMFRLI FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA* YNLN*I*QF*YKMCHFVLCMSE*SYNICLPIAGF\LWNMDKYTM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			IRKLEGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM EPGHLFPPPTPIFAGGANDRWVRSVSFSHDGLHVASLADDKMVR FWRIDEDYPVQVAPLSNGLCCAPSTDGSVLAAGTHDGSVYFWAT PRQVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH DLVGKDCRD\GYYEAEFGQE\RRP\LFPQN\LGIRCVKKKEVKE A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLNFRVFLPDG HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVPK TPPYCKAITEPVTVKMQLRRPSDQEVSESMDPRYLPDEKDTYGN KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR SGNTNPLSSFSTRTLPSNSQGIPPPLRIPVGNDLNASNACIYNN ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSSMSAGANSNTT VPVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY SGIGSMQNEQLSDSFPYEFFQV
5907	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPVPQPAKQNGK KATSKVPSAPHFVHPNDHANREAELKKKWVEMREKQQAAREQE RQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFPQLDDEATRK AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNL NRCSVPVDQASESLLKSKACFGAENLMRVLGNYCRLGEVRTHIR VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC NLEEISNYYGVSGFQTTEHFLTAVAHRLGKKKKGGLYSQEQAAK AVLADWVSGKISFYIPPPATHTLPTHLSABIVKEMTEVFDIEDT EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVGD
5908	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPSPSLPSEEETHPHTRA HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER* GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VTLWGKVVSSANHHXAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PAIPGSTIYWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHNDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICPKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMQLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEEEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRPSSVDSAKISESTVFSSQDD EEEENSAFESVPDSNQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GGGGSDSEABSSQSSLDLRREGSLSPVNSQKITLLLQSPAVKFI TNPEFPTVLHANYSAYRVFTSSTCLKHMILKVRRDARNFERYQH NRDLVNFINMFADTRLELPRGWEIKTDQQGKSFFVDHNSRATTP IDPRIPLQNGRLPNHLTHRQHLQRLRSYSAGEASEVSRNRGASL LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFLRQPNIFEMLQE RQPSLARNHTLRKEKIHYIRTEGNHGLEKLSCDADLVILLSLPEE EIMSYVPLQAAFHPGYSFSPRCSPCSSPQNSPGLQRASARAPSP YRRDFEAKLRNPYRKLEAKGFGQGPGKIKLIIRRDHLLEGTFNQ VMAYSRKELQRNKLYVTFVG3EGLDYSGPSRERFFLLSQELFNP YYGLFEYSANDTYTVQISPMSAFVENHLEWFRFSGRILG\LALI HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDEEFHQSLQW MKDNNITDILDLTFTVNEEVFGQVTERELKSGGANTQVTEKNKK EYIERMVKWRVERGVVQQTEALVRGFYEVVDSRLVSVFDARELE LVIAGTAEIDLNDWRNNTEYRGGYHDGHLVIRWFWAAVERFNNE QRLRLLQFVTGTSSVPYEGFAAPPWEPMGLRRPLP*KKWGKITS LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTFGT
5910	1526	446	VAEFAAMEPGRTQIKLDPRYTADLLEVLKTNYGIPSACFSQPPF AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLYKNTLCP IKRRTLLNKSSAPTVVSVLCCFGLWIPRSLVLVENTITSPYAVC FYLLMLVMVEGFGGKEAVLRTLRDTPMMVHTGPCCCCCPCCPRL LLTRKKLQ\R*CWALSNTPS*R*R*PWWACPSSPTASMTQQTFL RGAQLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKP ALFQVLLILTALQPSIPSVLANGGQIACSPPYSSKTRSQVMNCH LLILETFLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRMM AWTMKGCCTH
5911	109	595	QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVP CGHRRGGAAFKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
5912	924	277	MILNKALMLGALALTTVWSFCGGEDIVADHVASYGVNLYQSYGP SGQYSHEPDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFLLQDQ VTSPSPPPE**DL*TAKVEQLGAMPEPLLKHWGARIPTTL
5913	45	1198	QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FPGLYCICKRPYPDPEDSIPDEMIQCVVCEDWFHGRHLGAIPPE SGDPQEMVCQACMKRCSFLMAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSRP CAGSSSESDLQTVFNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED
5914	960	124	NLGGSELPPEEALPIQVASWNQRRVDPVLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRPTYGHAGTIYKDPVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACPIAP*SLGQRTRKRKAKARGTRTQASDPSCASWDH PHRHLPGLCRPAATS
5915	1604	703	FPGRPTRPLKLGRRRKRARIYQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSPPCPT PQEDPPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGPSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQQLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEPPEGL**AAGPAAH
5916	256	633	SPRMWEIWGPWHRWESPSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA
5917	1343	827	AHQILTYLEP/ICLVVNYNKILTVPLTKSVLEI*KPIHTPQTYR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			F*NDPPGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDQ FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLEKAYFRNAGNP HLEVIEETILALQSDRDQDVSPFAALEPKRRNIIDTAVLEKQN
5918	13	1247	EGAQVARRRSRRQWRAGRCGRGRGGRRAERTGGRGPPGRPRPLP PGPARRGRRRMETPFYGDEALSGLGGGASGSGGTFASPGRLFPG APPTAAAGSMMKKDALTLSLSEQVAAALKPAPAPASYPPA\ADG APSAAPPDGLLASPDLGLLKLASPELERLIIQSNGLVTTTPTSS QFLYPKVAASEEQEFAEGFVKALEDLHKQNQLGAGRAAAAAAAA AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL RGGAAT\VAPAAEPVPFPPPPPPGALGPRRP/RLALQGRRPQTV PDVP\SPGESP\PLSPIET\DTPRRI\KAKRRRL\RNPQIRAPK PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLK QKVLSHVNSGCQLLPQHQVPAY
5919	1	4254	TSVQGDSQGTPTSSQGSINMEHWISQATHGSTTSTTSSSSTQSG GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST GSRTAPKYGNAELMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP LREPFVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEQLGVVTNW PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM KVAYSILHKLGTKQEPMVRPGDRVALVFPNNDPAAPMAAFVGCL LAEVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHKG LPKSPTGEIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDAN NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCQALTQACGYTEAE TIVNVLDFKKDVGLWHGILTSVNNMMHVISIPYSLMKVNPLSWI QKVCQYKAKVACVKSRDMHWALVAHRDQRDINLSSLRMLIVADG ANPWSISSCDAPLNVFQSKGLRQEVICPCASSPEALTVAIRRPT DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG AIMCSVKPDQVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKNT PEVFAMTSSGAPISEYPPIRTGLLGFVGPGGLVFVVGKMDGLMV VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI VAEQRPDSTEEDSFQWNSRVLQAIDSIHQVGVYCLALVPANTLP KTPLGGIHLSETKQLPLEGSLHPCNVLMCPHTCVTNLPKPRQKQ PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRAEKIAVML MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVR TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV KMSHAATSAPCRSIKLQCELYPSREVAICLDPYCGLGFVLWCLC SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL CTKGLGSQTESLKARGLDLSRVRTCVVVAEERPRIALTQSFSKL FKDLGLHPRAVSTSFGCRVNLAICLQGTSGPDPTTVYVDMRALR HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSH LGEIWVHSAHNASGYFTIYGDESLQSDHFNSRLSFGDTQTIWAR TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID IETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQEALDLVPLV TNVVLREEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ LDPIYVAYNM
5920	1381	1499	QLGAVAHAGVSRIPP*LFPPLHPTFLSLNCLHHKLP/HPPGASM VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGP SGVGCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL LLMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH
5921	727	157	VCPGTGGE*GLWGQLGGLPKETPLKPMDAPTGSGLKRKFDDVDV GSSVSNSDDEISSSDSADSCDSLNPPTTASFTPTSILKRQKQLR RKNVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD GLTLDDVSDEDIDVENVEVDDYFFLQPLPTKRRRALLRASGVHR IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSQAGIKCQVD RMSPPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR Q\GAAQQPQ*GALPDCQLQPDRSTGL*DPSWIGSKGLSPTGKG AAATHLILLRVIENRGAEGKRK
5922	2475	495	SYSNWGLPPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CLYNATQYKVCSPRNDRPDACYNPSEPAATTVFEIRTGLLLSDT SKIITRTEEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS* RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLQKGEAN PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPQVVI LIKGEVHKCSPKPVPQTPYEELNLPAPELLKKTKNLFLQLAENV IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPI*KAE ASNP*VLKTSIIRQYCIARESGKDFIIPVGKPNCIGQKLYNSTTK TIT**DLNHTEKNPFSKFSKLKTA*AHAESH*DWTVPSGLV*IC RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGPSVYASR EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP IQVWHKFDPESLPGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE NSH
5923	137	638	QLCGRRGQRFRTSIKRMRPI*RTCPNTNL/IILLSQENTQIRDL QQENRELWISLEEHQDALELIMSKYRKQMLQLMVAKKAVDAEPV LKAHQSHSAEIESQIDRICEMGEVNRKAVQVDDDQFCKIQEKLA QLELENKELRELLSISSESLQARKENSMDTASQAIK
5924	274	2146	EKGKVKDAGAEQWISLSLSCKGSWETQYSNHLNSLTPPTSVRRM PLITTVTLLKMVARHHMKLLCSKAPSTQLQQKIFLHSQMGIHHQ SVCMKLKPNTSHIISILNGQPMALVQLETLAPLTIIIQKFQTQD HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPEIKLKITKTIQNG RELPESSLCGDLLNEVQASE\Q*NQSIESRKEKRKKSNKHDSSR SEERKSHKIPKLEPEEQNRPWERVDTVSEKPREEPVLKEGSPSS ANTIFCSNNGSVHW\PKFQVGDLVWSKVGTYPWWPCMVSSDPQL SVHTKINTRGARETHVQFFSNQPERAWVHSKRVREYKGHKQYEE LLAEATKQASNHSEKQKIRKPRPQRERAQWDIGIAHAEKALKMT REERIEQYTFIYIDKQPEEALSQAKKSVASKTEVKKTRRPRSVL NTQPEQTNAGEVASSLSSTEIRRHSQRRHTSAEEEEPPPVKIAW KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIEQVFALQNATG DGKFIDQFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS VSSPEATSGGTGSVEKKQQRRSIRTRSESEKSTEVVPVKKKIKKE QVQFLHVES
5925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPDPEIFRQRFRRPCYQNTFGPREALSRLKELCHQWLRPE INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALPT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAP PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEPGEKRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSPSLGSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5926	2	233	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEEPPGAIEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
5927	4146	1248	KHFSKPGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKRRILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWQKSPTDSVLKILGEAE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEPSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPPFHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GEIASECECDSVFNHLEELRLHLEQEMGFEKFPEVYEKIKAIHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYERSKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSBEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTPEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPEPSEASPQMSLKLEGNLEEPDDLETEILQEPS GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVSEDG VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPPFHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD GEIASECECDSVFNHLEELRLHLEQEMGFEKFPEVYEKIKAIHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5929	3	1558	LDFSWTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\ AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI LFHDPAVTLVKDFHVDTIVFPTAMMNVLPHLSAVEFHSAWAMGM RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS QLDSHPSHSAVVNWTSYASSIEALSSGNKEPKGTVFFDEPTFVK LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYALGAFDGLHTVE GRYYLQICTLLKCKTTNLNTCGDSAETASTRFEMPSLSGTFGTQ YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGR LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW
5930	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKPSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NAIPKGPMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAERE KETKALSLARALEEALEAKEEFERQNKQLRADMEDLMSSKDDVG KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK DYQRELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR QQLERQNKELKAKLQELEGAVKSKFEATISALEAKIGQLEEQLE QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE
5931	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKPSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGPMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE KETKALSLARALEEALEAKEEFERQNKQLRADMEDLMSSKDDVG KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK DYQRELEEARASRDEIPAQSKESEKKLKSLEAEILQLQEELASS ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE
5932	33	572	RHLEEICFLPLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG PGATLAVGLTIFVLSVVTIIICPTCSCCCLYKTCRRPRPV\APP PHPP/PVVHAPYPQPPSVPPSYPGPSYQGYHTMPPQPGMPAAPY PMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYNPAYMDA PKAAL
5933	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK APSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNRETNNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMPKNGSFWRPPPLNPYLHGMSEEQ ETEAPVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELRAQAVTTSKWELFD QHEESEEEENQNQEEESEDEDTQSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSP QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSRSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFPKKAVTYWKCDLF LCPERSVF
5934	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK APSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNRETNNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMPKNGSFWRPPPLNPYLHGMSBEQ ETEAPVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLDATEDSKKNEPIFKVAPSKWEAVDESELRAQAVTTSKWELFD QHEESEEEENQNQEEESEDEDTQSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSP QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSRSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFPKKAVTYWKCDLF LCPERSVF
5935	3	4493	SYWLSGWRLSRPPRQFWAGWRGYGRPGTMAPVHGDDCEIGASAL SDSGSFVSSRARREKKSKKGRQEALERLKKAKAGERYKYEVEDF TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRASFAG DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD KESEPAEEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS VQEVQVDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLF GKVWIESAETHVSCCVMVKNIERTLYFLPREMKIDLNTGKETGT PISMKDVYEEPDEKIATKYKIMKPKSKPVEKNYAFEIPDVPEKS EYLEVKYSAEMPQLPQDLKGETFSHVPGTNTSSLELFLMNRKIK GPCWLEVKKSTALNQPVSWCKVEAMALKPDLVNVIKDVSPPPLV VMAFSMKTMQNAKNHQNEIIAMAALVHHSFALDKAADKPPFQSH FCVVSKPKDCIFPYAPKEVIEKKNVKVEVAATERTLLGFFLAKV HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKIGRLKRSNM PKLGGRSGPGERNATCGRMICDVBISAKELIRCKSYHLSELVQQ ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC ELNVLPLALQITNIAGNIMSRTLMGGRSERNEFLLLHAPYENNY IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVL DPKVGFYDKFILLLDFNSLYPSIIQEFNICFTTVQRVASEAQKV TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYAKPLAALVT YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLEEVFKL GNKVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV ENIQKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP HVHVALWINSQGGRKVKAGDTVSYVICQDGSNLTASQRAYAPEQ LQKQDNLTIDTQYYLAQQIHPVVARICEPIDGIDAVLIATGWEL \DPTQFKVHHYHKDKENDALLGGPAQLTDEEKYRDCERFKCPCP TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK LKKQPFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV KS
5936	1124	139	RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKREADSSGLAFAS NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD SSDLVIENRQPPSSNGLSQQPPCWDLHPGCRHPGTRSSLPSLDD QEQASSGWGSRIRGDSGPSL
5937	31	1600	PTSLLKSTVQLMCRLLQDKRYQCVYSLKEIFKVLASFYVILVIL YGLTSSYSLNWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAPI LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LELISCDLERIPHSIFSLANNLHELDLRRNNLKTVEEIISFQHLQ NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLPL CTKLHYLDLSYNHLTFIPEEIQYL\SNLQYFAVTNNNIEMLPDG	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LPQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL PPELEGCQSLKRNCLTVEENLLNTLPLPVTERLQTCLDKC
5938	395	1865	YKGEGFFCNQEARGERKKKKKAMSSPNIWSTGSSVVSTPVPSQK MTVWILLLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME YTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNPP MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQFSF VGLRNTTEVVKTTSGDYVVMSVYFDLSRRNGYFTIQTYIPCTLI VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS YVTAMDLPVSVCFIPVFSALVBYG\TLHYPVSNRKPSKDKDKKK KNPAPTIDIRRPRSATIQMNNATHLQERDEBYGYECLDGKDCASF PCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIR FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGEGS LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA VDANASESP
5940	145	717	RRSASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEPANSNDKDDQV LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT LA\VYLVQMVVLILI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA WGQCNAPEW\LPFARPTNLTDEFEPPIGTYLNYECRPGYSGRPF SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVIHVIKGIQFGSQ IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDW SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV LFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQP PFASPTIPINDFEPPVGTSLNYECRPGYPGKMFSISCLENLVWS SVEDNCRRKSCGPPPEPPNGMVHINTDTQFGSTVNYSCNEGFRL IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVW SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPG FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQ DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKS CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRSASHCV LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDIPYGKE VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPAPRCEL PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGYLLVGK GFIFCTDQQIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHY GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRTHDALI VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAIHLHSQ GGSSVHPRTLQTNEENSRVLP
5942	4509	688	YLVRMRANPLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRKL DK\AQMIRPEERTGYFSSTDLGRTASHYYIKYNTIETFNELFDA HKTEGDIFAIVSKAEEPDQIKVRSEEIEELDTLLSNPCELSTPG GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAARIVRA LFEIALRKRWPTMTYRLLNLSKAIDKRLWGWASPLRQFSILPPH MLTRLEEKKLTVDKLKDMRKDEIGHILHHVNIGLKVKQCVHQIP SVMMEAFIQPITRTVLRVTLSIYADTWNDQVHGTVGEPWWIWV EDPTNDHIYHSEYFLALRKQVISKEAQLLVFTIPIFEPLPSQYY IRAVSDRWLGARAVCIINFQHLILPERHPPHTELLDLQPLPITA LGCKAYEALYNFSHFNPVQTQIFHTLYHTDCNVLLGAPTQSGKT VAAELAIFRVFNKYPTSKAVYIAPLKALVRERMDDWKVRIEEKL GKKVIELTGDVTPDMKSIAKADLIVTTPEKWDGVSRSWQNRNYV QQVTILIIDEIHLLGEERGPVLEVIVSRTNFISSHTEKPVRIVG LSTALANARDLADWLNIKQMGLFNFRPSVRPVPLEVHIQGFPGQ HYCPRMASMNKPAFQAIRSHSPAKPVLIFVSSRRQTRLTALELI AFLATEEDPKQWLMMDERMENIIATVRDSNLKLTLAPQIGMHH AGLHERDRKTVEELFVNCKVQVLIATSTLAWGVNFPAHLVIIKG TEYYDGKTRRYVDFPITDVLQMMGRAGRPQFDDQGKAVILVHDI KKDFYKKFLYEPFPVESSLLGVLSDHLNAEIAGGTITSKQDALD YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKSLIELE LSYCIEIGEDNRSIEPLTYGRIASYYYLKHQTVKMFKDRLKPEC STEELLSILSDAEEYTDLPVRHNEDHMNSELAKCLPIESNPHSF DSPHTKAHLLLQAHLSRAMLPCPDYDTDTKTVLDQALRVCQAML DVAANQGWLVTVLNITNLIQNVIQGRWLKDSSLLTLPNIENHHL HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVFSSMVBS ELHAAKTKQAWNPLSHLPEINVGISVKGSWDDLVEGHNELSVST LTADKRDDNKWIKLHADQEYVLQVSLQRVHFGPHKGKPESCAVT PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHHVASLSFYT PEIPGRYIYTLYFNSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ GL
5943	1	2274	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGELFLWD GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFBIYQVL LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIILSBABEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVBLELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ KKKQLEDLSYCREERKSLREMAERLADKYEEAKEKQEDIMNRMK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KLLHSFHSELPVLSDSERDMKKELQLTPDQLRHLGNAIKQVTMK KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV KQINDIRNHVNF
5944	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS KKQPSVLVTPPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES TRQATQLINALIKDPDKEIDELIPKNRLKSSSANSKIGSSAPTT TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP VN\NVRPGFPVSFP\LAYPPPQFAHALLAAQTFQQIRPPRLPMT HFGGTFPPAQSTWGPFPVRPLSPARATNSPKPHMVPRHSNQNSS GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLP VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSSP SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPPVVET TNTRPPNSSSSSGSSSAHSNQQQPPGSVSQEPRPPLQQSQVPPP EVRMTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLPENSPT SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG TSAPSVIGSNLSTSVGHSGIWSPEGIGGNQDKVDWCNPGMGNPM IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
5945	1461	197	GVTHLFLPGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA QEGDLPELRRLLEPHEAGGAGGNINARDAFWNTPLMCAARAGQG AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRREE\KDRAWERDLRTYMNLEF
5946	541	1666	ILGSVSSIQPEEVS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\SHLQPDVLVHAVLRVVDF/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL
5947	3	1317	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKER CEGPELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACPVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGSIYVMVNDKPVCKPCYVKNHAVVCQGCRNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS
5948	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP PVCLRTKRHKNNRVKKNEALPSAHGTPASASALPEPKVRIVEY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE KRKGDCVPAVSQSMPEFLMDRFEKESHCENQKQGEQQSLIDEDA VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/ RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI QCHKANCYTAPHVTCAQKAGLYMKMEPVKELTGGGTTPSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR KKAKKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGPEEDGAAL GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL TNGPGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFPFDNKRSWQ WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL SRVHGEPTSDLSDID
5949	39	3370	YRERYPVSGGSVLRSALEVCNDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP PVCLRTKRHKNNRVKKNEALPSAHGTPASASALPEPKVRIVEY SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/ RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI QCHKANCYTAPHVTCAQKAGLYMKMEPVKELTGGGTTPSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR KKAKKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM KAAKEKLKYNQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDIII KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGPEEDGAAL GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL TNGPGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFPFDNKRSWQ WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL SRVHGEPTSDLSDID
5950	1166	373	ESRSLTMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ DQRRLLQSCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP SSSGDSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLEPWCPAAQGR LTRVLLTASTLKSIPTSLLGDLPFRPIIGDVDIAGLLGDMLLLR
5951	143	5449	WNVKFSLLVVQLFKFSDKEEHEQNDSISGKTGETGVKEMIATRK VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV GLPSCVDEVTECNLELKDTMGIADKTENTLERNKISPLGYCEDA ESNRQLESTEFNKSNLEVVDTSTPGPESNILENAICDVPDQNSK QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP VIHSKQNMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK QCHKPQQQAPAMKTNSHVKBELEHPGVEHFKEEDKLKLKKPEKN LQPRQRRSSKSPSLDEPPLPIPDNIATIRREGSDHSSSFESKYM WTPSKQCGPCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK YKNKYRSLMFNLKDPKNNILPKKVLKGEVTPDHLIRMSPEELAS KELAAWRRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE AESIADALSSTSNILASEFPEEEKQESPKSTFSPAPRPEMPGTV EVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKEIPPLNEQ TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSAEIETSVVG SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE VGNTCPSEPPSKSITFTSRSTSPRTSTNFSPMRPQQPNLQHLKS SPPGFPFPGPPHFPPQSMFGFPPHLPPPLLPPPGFG\FA\QNPM VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPE RRHSDPWGRQDQQQLDRPPNRGKGDRQRFYSDSHHLKRERHEKE WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD GKASRDSRNVDKKPDKPKSEDYEKDKERESKSHREGEKDRDRYH KDRDHTDRTKSKR
5952	3226	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIP ASDACKNVTLHVPSKLDAEKLVGRVNLKECPTAANLIHSSDPDF QILEDGSVYTTNTILLSSEKRSPTILLSNTENQEKKKIPVFLEH QTKVLKKRHTKERVLRRAKRRWAPIPCSMLENSLGPPPLPLQQV QSDTAQNYTIYYSIRGPGVDQEPRNLPYVERDTGNLYCTRPVDR EQYESFEIIAFATTPDGYTPELPLPLIIKIEDENDNYPIPTEET YTFTIPENCRVGTTVGQVCATDKDEPDTMHTRLKYSIIGQVPPS PTLFSMHPTTGVITTTSSQLDREIIDKYQLKIKVQDMDGQYFGL QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL NYEEKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL TDPTGWVTIDENTGSIKVPRSLDREAETIKNGIYNITVLASDQG GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAEIVAVDP DEPIHGPPFDPSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG GGVQLGKNAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAQGVCGTVGSG IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC RYTYSEWHSFTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPFKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL PEPSIRSVMQKYLAERNEITFDKIFNQKIGFLLFKDFCLNEINE AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIFQKFN ESDKFTRFCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRK ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYA TEIILGLEHMHNRFVVYRDLKPANILLDEHGHARIS\DLGLACD FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADWFSLGCMLFKLL RGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPELKSLLEGLL QRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVYLQKYPPPLIPP RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW QQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM HGYMLKLGNPFLTQWQRRYFVLFPNRLEWRGEGESRQNLLTMEQ ILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNE TFKEAQRLLRRAPKFLNKPRSGTVELPKPSLCHRNSNGL
5955	1726	444	KRERERFRLAVCPLRYPSAYESSPGTELRECGLCRSGQEFADCRR PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ VWKRCINIWRDVGLFGVLNEIANSEEEVFEWVKTASGWALALCR WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILINTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRVWEAQMWTCE3WPTLSGRCQTGCWSPD GSRLLFTVLGEPLIYSLSPPERCGEGKG\ALEVQSQQRLWQICL RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL
5956	1705	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGPSVAQKPPGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCPVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSRSPLLNHLSDVHNGIAELLVNGKTEIALEAT QLLLKLLDPQNREFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTSKTTKDS LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIPIEHPGD
5957	1479	451	ELQVAVAMDTLDRVVKPKTRKARPLEKREPKLNENIKNANLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLPMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLLKKSGCRTPRIE LEEMQPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KQLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL
5958	1	3138	AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHYPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAVAEPSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMERESFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRPAVPRLEKTNMSINFDLQIRSS NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWSPEE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EPHKEEEVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEPL LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG GESAVLKVRSRLWAHTPLQRKNDPVALASLVSFEVKKMPYTDQP AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY NVKSVCSRERGGSGIRSVSPYEHIITVGTGQGSLLFYDIRAQRFL EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF FPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
5960	2853	870	PVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE LDWASINGFCEQLNEDPEGPPLATRLLAHKIQSPQEWEAIQALT VLETCMKSCGKRPHDEVGKFRPLNELIKVVSPKYLGSRTSEKVR NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG SSEDL\MKEL\YQRCERMRPTLPPTGRVDTEDND\EALAEILQA NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRPPAQTSLP ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP LESIKPSNILPVTVYDQHGFRILFHPARDPLPGRSDVLVVVVSM LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET WGSL
5961	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS FYTQWGNQETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYPTRYAKCILMENSPGADFEVWFYDGVKI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR ICLALESIISEEERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNEGLGLTT TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL ESKYGFQEQLLYSVLESLVNSGRLRGTVVGGRQDKAVFVPDIYS RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK KKPEISFMPQDEIEDPLRKHIQDAPEEFISELAEYLIKPLNKTY LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVGNLYNNIRLPEKG MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA AEACDIMVKRGDKKRERQILFQHRQALAEQLKVTEDPALILHLT SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELQELSS SIKDLVLKSRKSSVTEE
5963	62	1130	PWNPQDPPGNRGLMG\QKGEYGPP\GQQGKKGAPGMP\GLMGSN GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP GVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPPGISKEG PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF RKGPNY
5964	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRPGGMEEACQVQTTK RGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMPIVAFQL FDKSGNGEVTFENVKEIPGQTIIHHHIPFNWDCSFIRLHPGHNR KKHLNYTEFTQFLQELEHARQAFALKDKSKSGMISGLDFSDI MVTIRSHMLTPFVEENLVSAAGGSISHQVSPSYFNAFNSLLNNM ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ LADLYNASGRLTLADIERIAPLAEGALPYNLAELQRQQSPGLGR PIWLQIAESAYRPTLGSVAGAVGATAVYPIDLVKTRMQNQRGSG SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAI KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEI VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG TAARVFRSSPQPG\VTLVTYELLQRGFYIDFGGLKPAGSEPTPK SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA VVQPKAAVAATQ
5965	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG CGSYCAGAKASPLPGKMAMGLMCGRRELLRLLQSGRRVHSVAGP SQWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA EVQVQAPPVVAATPSPTAVPEVASGETADVVQTAARQSFAELGL GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV TGQREAARIIHNHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL YQKKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQTG GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP AVRTVLKIPQRVVHDLDKLPPREGFLESFKKGWKNAEMTRQLRE REQRMRNQLELAARGPLRQTPTHNPLLQPGKDNPPNIPSS\SSS SSKPKSKYPWHDTLG
5966	102	1925	RSKQVMARLTKRRQADTKAYQHLWAAIETIRNQKQIANIDRITK YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCPRVYHSKCL SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE FKADAQLLLHNTVIPYGADSEQADIARMLYKDTCHEL\DELQLC KNCFYLANARPDNWPCYPCIPNNHELDWAKMKGFGFWPAKVMQKE DNQVDVRPFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGNKKA CDELELHQRFLREGRFWKSKNEDRGEEEABSSISSTSNEQLKVT QEPRAKKGRRWQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
5967	102	1925	RSKQVMARLTKRRQADTKAIQHLWAATEIIRNQKQIANIDRITK YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE GYWLPGDEIDWETENHDWYCPECHLPGEVLICDLCFRVYHSKCL SDEPRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA CDELELHQRFLREGRFWKSKNEDRGEEEAESSSISSTSNEQLKVT QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF KDRNKSDHKRETERVVRFALEKLRSEMEEEKRQAVNKAVANMQG EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
5968	81	1288	VRFPRRGGAPPTVLTPGRQQGVFLGPQRPGSEPDIPARGQPHPP RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLAGTSLSVLNVYL ENWLPVSYVPYYLPCPEIFNMKLHYKREKPLQPVVWSQVPQPKL LEHRPTQLLTLTPWLAPIVSZGTFNPELLQHIYQPLNLTIGVTV FAVGN/HFLESAEEFFMRGYRVHYYIFTDNPAAVPGVPLGPHRL LSSIPIQGHSIWEETSMRRMETISQHIAKRAHREVDYLFCLDVD MVFRNPWGPETLGDLVAAIHPSYYAVPRQQFPYERRRVSTAFVA DSEGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWR EESHLNRHFISNKPSKVLSPEYLWDDRKPQPPSLKLIRFSTLDK DISCLRS
5969	1126	503	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKQRRIAANKCLC TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
5970	316	4712	SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDVVDKEKAIA KALEDLRANFYCELCDKQYQKHQEFDNKINSYDHAHKQRLKDLK QREFARNVSSRSRKDEKKQEKALRRLHELAEQRKQAECAPGSGP MFKPTTVAVDEESGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKRKKRKRKKNKSSAPADSRRGPKPEPPGSGSPA PPRRRRRAQDDSQRRSLPAEEGSSGKKDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EXIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYPGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP GSSDALFGHQPP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHPDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, N=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TPEEMEKYSKLQQAAQQHIQQQLLAKQVKAFFASAALAPATPAL QPIHIQQPATASATSITTVQHAILQHHAAAAAAAAIGIHPHPHPQ PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATPLASHPIHIIPA SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI FSGQDLQHPPSHQT
5971	53	2149	SPLYPVGVDMDNPIGNWDGRFDGVQLCSPACVESTYLLRINDIY PESVTQERRPPKLAPMSRGVGDKGSSSHNKPKATGSTSDPGNRN RSILFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTD FDRSSPPLQPPPVNSLTTENRFHSLPPSLTKMPNTNGSIGHSPL SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENP PFYGVIRWIGQPPGLNEVLAGLELEDECAG\CTDGTF/REGTRY PTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAIWBAY LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF CLFAPSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYG YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRV EPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSPIN SNLKPAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT PRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHP KRLNHKYNPVSLPKDLPDWDWRHGCIPCQNMELPAVLCIZTSHY VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYL KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
5972	440	1761	ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPSAMTQ EPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAGSCI PSAIVSFTVSRRNANVIPNFQILFVSTFAVTTTCLIWPGCKLVL NPSAININPNLILLLLLELLMAATVIIAARSSEEDCKKKKGSMS DSANILDEVPFPARVLKSYSVVEVIAGISAVLGGIIALNVDDSV SGPHLSVTFFWILVACFPSAIASHVAAECPNKCLVEVLIAISSL TSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLLLLLLLV LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPGWGG GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH NP
5973	65	2007	NGDGKDLFGHIWAWRSNGIYSNFRRSPHAGMAEDEPDAKSPKTG GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE HTDTCLPKQSVYDAYRKYCESLACCRPLSTANPGKIIREIFPDI KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP EVTPAPRDELVEAACALTCDWAERILKRSPSSIVEVARFLLQQH LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANNLQV NALVARLPLLLPRAPRSLIPPIPVSPPILAPRLSSGALKVATLP LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTQPR GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGQAPPAKAAKQD IEDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL PWETWGSGGEGNSAGGAERPGPMGEAEKGAVLAQG\QGDGTVSK GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV DTAPQGNKDLKEHVLQSSLSQEHKDPKATPP
5974	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVENIENGDTKGK\BID LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR TV\ASIKNDPPS\RDNRVVGSARARPSQPPEQFSSAQQNGSV\S DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKRKRRLQQQELR EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC VCVKRKPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK ECIRALGRNKPHTPPRASKLTQVLRDSFIGENSRTCMIATISPG MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5975	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR TV\ASIKNDPPS\RDNRVVGSARARPSQPPEQPSSAQQNGSV\S DISPVQAAKKEPGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVPQIILRR KGKLHGKPSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK ECIRALGRNKPHTPPRASKLTQVLRDSFIGENSRTCMIATISPG MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5976	20	2945	VHHLHLTRVSVVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LEF PEVSWMEVKDDNMKGAMLTNTGKYAIPTIDA\EAYAIGKKEKPP FLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD ECIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE TGYTKRLRKQLPSPPPPIPPPRPLIQRNLQPLMRSPISRQQDPL MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT ATVSISVHSEKSDGPFRDSDNKILPAAALASEHSKGTSSIAITA LMEEKGYQVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGG RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT QGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPQPSPQFPP GQP\PPAGYSVPPPGFPPAPANLSTPWVSSGVQTAHSNTIPTTQ APPLSREEPYREQRRLKEESKKKSKLDEPTNDPAKELMEYKKIQ KERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRSRSYSRSFS RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPPPYDM KAYYGRSVDFRDPPEKERYREWERKYREWYEKYYKGYAAGAQPR PSANRENFSPERFLPLNIRNSPPTRGRREDYVGGQSHRSRNIGS NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKHRKRR KGRESEGFLNPELLETSRKSREPTGVESNKTDSLFVLPSRDDAT PVRDEPMDABSITPKSVSEKDKRERDKPKAKGDKTRRKNDGSAV SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE EGLFQRCQIRKANN
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGH/REYLT PVLKESKPKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKVK AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAIIEEDDGDGGWV DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEEDEDEG EAADMEEYEESGLLETDEATLDTRKIVEACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFGYDEQRQPLTVEHMYEDISQDH VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL GVHMYLLIPLKFVQAVIPTIRYDYTRHFTM
5978	160	3213	RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQLDTLQ LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEVERNV EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR VEMVHQSCNDPTKNIIREFASDPEVGECWGYNRFPRLDLLANEG YLNRQNDTVILRPQVRSPTPFQKSRDQHWYITQLEAAQTSYIQQ INNLKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CSDWLLER\GDVSAS\VREAKEDEEDEEKIQNEDYHHELSDGDL DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDEETMSGENDV EYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTQMAEVRCMKTDVKN TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLQDLGME LLAKSSVANCYIRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE NSRSKGDCQTLSEGSPGSSQSGSRHSSPRALIHGSIGDILPKTE DRQCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGHLEGL QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE QEEHTSVGGPHDSFMVMTQPPDEDTHSSFPPDGEQIGPEDLSFNT DENSGR
5979	212	3665	LPDMTMYLWLKLLAFGFAFLDTEVPVTGQSPTPSPTDAYLNASE TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK LFTAKLNVNENVECQNNTCTNNEVHNLTECKNASVSISHNSCTA PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC DTQNITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNSHK FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTPK AYFHNGDYPGEPPILHHSTSYNSKALIAPLAPLIIVTSIALLVV LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRLPLAEFQSIPRVFSKFPIKEARKPFNQNKNRYVD ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT RAPGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI LIHQALVEYNQFGETEVNLSSLHPYLHNMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEEPSKYINASPIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS
5980	3	2363	DAWGCKLRRLRPTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSPP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTPHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLMLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEPHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST
5981	1	2519	GRRHSAAMERPWGAADGLSRWFHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV ILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TEPGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT RDPIYPTGLASEPGARSMNISINGFTESFLTSQWVSYTIDFKDI LERNCEEKDYTIWIAHSTDPEDYEDGCILGYKEQPLRLRKSSVC QNGRDYVVTKQPSICLCSLEDFLCDPGYYRPENDSKCVEQPELK GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC GGRFLVHLYSVLQQI\AEA\NGVDGVDALDTASHTNKSGYHDDS DEDLLE
5982	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK GCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMQIPR FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALTSKPYAF TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV AGMLQSPQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEE VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRM TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF LLGADGGCITRQDLPKDCFIIYQQHHGDVGAPIADVILPGAAYT EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA VEEPSIC
5983	248	1763	EARGDGGRRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG RQ\YSAAIALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIQ DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC GLQLANDSVNRLSRILMELDGPNWREKLGLIPAVPASVFLQAWH PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK DALSKYSECLKINNKECAIYTNRALCYLKLCQFEEAKQDCDQAL QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK MELEEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPGRPA GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL SDTPNNHFTLEDIQALKRQYEL
5984	755	1193	SSVCNACTYVSNLGKKQRSVSPLASGLMRVSTGPELRLHHSFVL TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG
5985	22	1408	RRVARFGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGEKIYKR/DGERIITQGE K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF GELALVTNKPRAASAYAVGDVKCLVMDVQAFERLLGPCMDIMKR NISHYEEQLVKMPGSSVDLGNLGQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5986	1806	484	DAWKSTSLTPHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG VKRWTKNVDIFNKELLLIPIELEVHWSLISVDVRRRTITYFDSQ RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL TV
5987	1806	484	DAWKSTSLTPHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL TV
5988	1292	410	FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ RLDCIYLNAGIMPNPQLNIKALLFGLFS\AEGLLTQGDKITADG LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC PGTALCNLTYGILPPFIWTLLMPAILLLRPFANAFTLTPYNGTE ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCL
5989	194	2610	AMEPFQHSQHVLEQLNQQRQLGLLCDCTPVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNABALAT EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ SAASGAEQTEKADAPREPPPVELKPDPTSGMAAAEAEAALSESS EQEMEVEPARKGEEEQKEQEEQEEEGAGPAEVKEEGSQLENGEA PEENENEESAGTDSGQELGSEARGLRSGTYGDRTESKAYGSVIH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTHSPLKPYGCEECGKSYRLIGLLNLRKKRHSGEARYRCED CGKLPTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNLKAHLKIHAIDGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADDGALQRHVRIHTG EKPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQQKAGIKILEPEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAE
5990	2	4700	PGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSIPDPP MHLACPEEEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DPVPNDLTPVDPVLVKSRPTDPRRGAVSSALGGSAFQLLVESES LDPPKTIIPEVKEVVDSLKIESGTSATTHEARPRPLSLSEYRRR RQQRQAETEERSPQPPTGKWPSLPETPTGLADIPCLVIPPAPAK KTALQRSPETPLEICLVPVGPSPASPSPEPPVSKPVASSPTEQV PSQEMPLLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS LPPPPLQPPSLPLSMGPVLPDPPTTHYAPLPSWPCYPHVSPSGYP CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTY GPLGWGPGPQHAPPWSTVPPPPLPPASIGRAVPQPKMESRGTPA GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKPVPASPHPK HKVSALVQSPQMKALACVSAEGVTVEEPASERLKPETQETRPRS KPPLPATKAVPTPRQSTVPKLPAVHPARLRKLSFLPTPRTQGSE DVVQAFISEIGIEASDLSSLLEQFEKSEAKKECPPPAPADSLAV GNSGGVDIPQEKRPLDRLQAPELANVAGLTPPATPPHQLNKPLA AVSLLAKAKSPKSTAQEGTLKPEGVTEAKHPAAVRLQEGVHGPS RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRWNVKRHQDI TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQADPSAPCLAPS SLLSPEASPCRNDMNTRTPPEPSAKQRSMRCYRKACRSASPSSQ GWQGRRGRNSRSVSSGSNRTSEASSSSSSSSSSRSRSRSLSPP HKRWRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSRSRSRS PSPRRSDRRRRYSSYRSHDHYQRQRVLQKERAIEERRVVFIGK IPGRMTRSELKQRFSVFGEIEECTIHPRVQGDNYGPVTYRYAEE AFAAIESGHKLRQADEQPFDLCFGGRRQFCKRSYSDLDSNREDF DPAPVKSKFDSLDFDTLLKQAQKNLRR
5991	334	1379	RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELYQELGLQAR DLRFQHVMSITVRNNRIIMRMEYLKAVITPSCLLILDYRNLNLK QWLFRELPSQLSGEGQLVTYPLPFEFRAIEALLQYWINTLQGKL SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI KIFKESILELDEEELLEELCVSKWSDPQVFEKSSAGIDHAEEM ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM RLNLQLTMQTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL
5992	2	609	AGPDFRLVCGVSGSGFPGGRQSQATEWRPLRPWNGAMEKLRRVL SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTNYSLSYIPYARDAVIKCCSSLLS
5993	1650	594	AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH
5994	394	1934	AGEVQLHVWIRGMRIQPQ/KAAAIIDLDDPREPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWHMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMNTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLNTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNPEPDP
5995	2	2437	RPPGPGPASGAWLCTRARGSAAPVPPLPRPPSRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL CSVGSLSDKEVETPEKKQNDQRNRKRKAEPYETSQGKGTPRGHK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ISDYPERRVEQPLVGLDGSAAKEATEEQSALPTLMSVMLAKPRL DTEQLAQRGAGLCFTPVSAQQNSPSSTGSGNTEHSCSSQKQISI QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ REEIERQRKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKHPPKISNK VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP PKPVVTPEAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV STSSPAGAAIASTSGASNNSGSN
5996	1612	981	DQQACLLGLMLTLEPGILEPDPSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5997	1612	981	DQQACLLGLMLTLEPGILEPDPSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQIS3VKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5998	1612	981	DQQACLLGLMLTLEPGILEPDPSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLYP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRSTVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLPQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENNDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAPS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP
6000	101	1561	TEPCRTAENCTATMSENNKNSLESSLRQLKCHPTWNLMEGENSL DDPEDKVFYRTEPQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCQGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGE
6001	176	1038	AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQPPHI WLHPDADGSGYLEQKELQNLIQELQQARKKAGLELSPEMKTFVD QYGQRDDGKIGIVELAHVLPTEENFLLLFRCQQLKSCE\EFMKT WRKYDTDHSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFNKA FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKKNI MALSDGGKLYRTDLALILCAGDN
6002	977	81	LAPPGGGLHIPPRTPLSHSRFPPSHHAPHPSPLPLPPADLHPHS SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKPFFCFLPNIINRT YFPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE ESDFEAAPSVGATGVITDYPTALRHYLDNHGPAARTS
6003	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDPI QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN LLKNQRTLSRVFLKRLCRIPTRMFADPHGKRVFSMFLETLVDPI QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD PINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSNGSPLTRPTP RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS PFNKSALKEAMPDDDADQFPDDLSLDHSDLVAELLKELSNHNER VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL NNSLPPPHPEN3EDPEEDLSETETPKLKKKKKPKKPRDPKIPKS KRQKKERMLLCRQLGDSSGEGPEFVEEEEEVALRSDSEGSDYTP GKKKKKKLGPKXEKKSKSKRKEEEEEDDDDDDSKEPKSSAQLL EDWGMEDIDHVFSEEDYRTLTNYKAPSQFVRPLIAAKNPKIAVS KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPGSPRVPDAKKPK PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV SDGSTSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV CQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI QWEAKEDNSEGEEILEEVGGDLEEEDDHHMEFCRVCKDGGELLC CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK S\RRRKNKDPKFAEMEERFYRYGIKPEW\MMIHRILNHSVDKKG HVIYLIKWRDLPYDQASWESEDVEIQDYDLPKQSYWNHRELMRG EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG TLHPYQMEGLNWLRFSWAQGTTTILADEMGLGKTVQTAVFLYSL YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE LITIDMAILGS:DWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGQITGNMRQEAIDR FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDSDWNPHNDIQ AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED SSVIHYDDKAIERLLDRNQDETEDTELQGMNBYLSSFKVAQYVV REEEMGEEEEVERETIKQEESVDPDYWSKLLRHHYEQQQEDLAR NLGKGKRIRKQVNYNDQSQEDRDWQDDQSDNQSDYSVASEEGDE DFDERSEAPRRPSRKGLRNDDKDKPLPPLLARVGGNIEVLGFNAR QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH PSMALNTRPAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP EPTPQQVAQQQ
6006	1	965	DNDPLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC GRFRHNTVIFILGKEHQLKRLHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEPPTEEVTCKEPILVVSYKVGV CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG SLAPRPCDVPTCPTL
6007	3	2351	HELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIK EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSQLEYYAS SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E EKLAAVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSECAEQLR QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLYNICPT SLPILIYGLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT ILGFSHAFIFFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM VITVTVKMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPP LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1089	AGVRRAGARRGPGRALPAGATAVPPFSARRRRRCPAPEHAGPAR ASRPSQETMFQLPVNNLGSLRKARKTVXKILSDIGLEYCKEHIE DFKQFEPNDFYLKNTTWEDVGLWDPSLTKNQDYRTKPFCCSACP FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLYEIVRKHIYREHFQHVAAPYIAKAGEKSLNGAVPLG SNAREESSIHCKRCLFMPKSYSALVQHVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPENVYSVHPEKEHKAEKVP AVANYIMKIKNFTSKCLYCNRYLPTDTLLNHMLIHCLSCPYCRS TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPVP TRREIEKLAASLMV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQNKNASENDERLSNPQIEKQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA
6009	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMPPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAPLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRCSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDELLWFGGR*LIIIG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			I**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVLGG AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQGP GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAAI CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHCL GSFPGRLWP*PFISQERPNGHCQWEPRLAVPSWKCRWSRWRVRG TWRYGNPLLNLL*GAWLGGAACGQQQGGPLSTWQACTGPGQAAF LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD
6010	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCSLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCWACRIASSKTANPVAKRHPVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGPQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKQTQACI TAATAVSGIIADLDTTIMPATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRPGTEC TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM LKKERELEEARKKLAQIRQQQQYKFLPTELRDDEG
6011	446	1835	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGGQPSLQDELKDNT TVPTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSPGPVSDH DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTRPARSVVVAED GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFVI QTYLPCIMTVILSQVSPWLNRESVPART VPGVTTVLTMTTLSIS ARNSLPKVAYATAMDWFIAVCYAPVPSALIEFATVNYPTKRGYA WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF GIFNLVYWATYLNREPQLKAPTPHQ
6012	351	5013	PAELFQSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGE EGIQVREIACIQKDKDIPAEDIICEYPEPKPLLEQACLIPCQQD CIVSEPSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEP QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE REKDRSKGVKDDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR EVMCINKTGKAADLSFCQQEKLPMTPQSCVITKECQVSEWSEWS PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS QGDGVVPCATYGWRITEWTECRVDPLLSQQDKRRGNQTALCGGG IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK ECGPGTQVQEVVCINSDGEEVDRQLCRDAIPPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWQQCIEDTSVSSFNTTITW KGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN GGRDCTDPLYESKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTPV NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA DDPSKVVDEEPCADIELIIDGNKNMVLEESCSQPCPGDCYLKDW SSWSLCQLTCVNGEDLGPGGIQVRSRPVIIQELENQHLCPEQML ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR ARPESNDQPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI DBVIIEQEVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCNSD EMPLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALED5Q9SFS ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ P
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRPVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIERESDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII F\KAMGQGLQDB\EQEKLLRICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE EKEVLPDQVEEEEENDDQEEEEDEDDDEDDEEEDRMEVGPFSTG QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL \SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLP
6016	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRPVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII F\KAMGQGLQDB\EQEKLLRICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKACQQEEQGSVNDVKEEEKE EKEVLPDQVEEEEENDDQEEEEDEDDDEDDEEEDRMEVGPFSTG QESPTAENARLLAQKRGALCGSAWQVSSEDVRWDTFP\LGRMPR SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL \SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLP
6017	203	3469	SHQEIEQNSAMAPRKRGGRGISFIFPCCPRNNDHPEITYRLRNDS NFALQTMEPALPMPPVEELDVMPSELVDEDLDLTDKHREAMFALP AEKKWQIYCSKXKDQEENKGATSWPEFYIDQLNSMAARKSLLAL EKEEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQ SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER TRPQTLINDLDKSTGRYRDEVSLKTAIMSPINAVLSQGAGVESL DFRLHLRYE\PLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE DELEFAKRFELVHIDTKSATQMFELTRKRLTHSEAYPHFMSILH HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN FNIKNVVRMLVNENEVKQWKSQAEKMRKEHNELQQKLEKKEREC DAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE LSRRAVCASIPGGPSFGAPGGPFPSSVPGSLLPPPPPPPLPGGM LPPPPPPLPPGGPPPFPGPPPLGAIMPPPGAPMGLALKKKSIPQ PTNALKSFNWSKLPENKLEGTVWTEIDJTKVPKILDLEDLERTF SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYPKK KFAERVAEVKPKVEAIRSGSSEVFRSGALKQLLEVVLAPGNYMN KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPQPGDKFVSWVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFQIFDQFLQAVSEAKQENENMRKKKEEEE RRARMEAQLKEQRERERKMRKAKENSEESGSEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLNP
6018	13	2510	TIGQSGGIRRRREAVWFEVVNMDFSRLHMYSPPQCVPENIGYTY ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIN ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVPKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDPMAPHQEHEVRMS HLEDILGKLRKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLPSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEH!PKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIPSNWGHPEYTCLYRPRVHGEPVK
6019	2	1066	TPNDREPPPQRPPSSRRASHLAQETTSAASLGDQTQILGSLTTA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PVITSAIRSMFGISSQILTNAQGQVIGTLPWVVNSASVAAPAPA QSLQVQAVTPQLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTQT QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN EAELRNQEGQQNLMEPVGGEPSKKRKRRTSFTPQAIEALNAYFE KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF QIP
6020	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT DFSDTFKLYRGKSDENEDPSVVGEPKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEGNFNWRFVFPPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV
6021	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT DFSDTFKLYRGKSDENEDPSVVGEPKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEGNFNWRFVFPPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV
6022	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT DFSDTFKLYRGKSDENEDPSVVGEPKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEGNFNWRFVFPPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SQELGMFVSLNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGQLVF LEGL/IVCSGR\VPQAQKEPHPLQPLRBANAGNLKPLFEFVREA LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT VCWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF AKGMSPAVL
6024	3	3260	PLSPLCYPRFRCLFCLQFAYIPASRMEQLNELELLMEKSFWEEAE LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVQNKEGNCEK RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW IIDKDPGYLILYPDMLISGTSIASSIRCMRRAVLSETFRSSDPA TRQMLIGTVLHEVFQKAINNSFAPEKLQELAFQTIQEIRHLKEM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFFQMQLSL PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKIDVTVGVKI HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSQERRADP EAGLLLYLKTGQMYPVPANHLDKRELLKLRNQMAPSLFHRISKS ATRQKTQLASLPQIIEEEKTCKYCSQIGNCALYSRAVEQQMDCS SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKN HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGQYLHNFQCKH GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKLMENTFVSKKLR DLIIDFREPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK VLLSKDYTLIVGMPGTGKTTICTLVRILYACGFSVLLTSYTHS AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI KS\LALLEELYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIIAP YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN KDGTVGELLKDWRRLNVAITRAKHKLILLGCVPSLNCYPPLEKL LNHLNSEKLIIDLPSREHESLCHILGDFQRE	
6025	3977	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA ARYGEAGEGPGWGGAHPRICLQPPPTSRTSPPPPRLPALEQGPG GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVQQWVSYADTELIP AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHTYLA GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRQ PEFRAVLGEVVLYSGARPLS:QPGPEAPALPKTAAQLKKEAKKR EKLEKFQQKQKIQQQQPPPGEKKPKPEXREKRDPGVITYDLPTP PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGPFKPEYGRPNVS AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQHLKGKNVIHPPLSRSI.PIVFDEFVDMDPGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMPPG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE KAAKEPGVSPDKISLQQDEDVLDTWPSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFPWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML	
6026	2674	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTPPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESPP SNLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KPIVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAPVK TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR KKCVNVTTKSLHPDQKEYEINNTTTLMACLGGLLGIIGVICLIS CLSPEMNCDSGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS TSLKVKATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYVDKDTTK PISFYLSSLEELLAWKPRLEDGFNVALEPLACRQPPLSSQRPRT LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVPVYFSHHTV TIPPVGWTNTAHRHGVCVLGSFITEWNEGGRLCEAFLAGDERSY QAVADRLVQIT\RFPRFDGWLINIENSLSLAAVGNMPPFLRYLT TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGP FTNYNWRIEEHLERNLGQQAGERRADVYVGVDVFARGNVVGGRFDT DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG DPVALRNRCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGEIBDLQQWLTDTERHLLASKPLGGLPETAKEQ LNVHMEVCAAFEAKEETYKSLMQKGQQMIARCPKSAETNIDQDI NNLKEKWESVETKLNER\KT\KLEEALNLA\MEPHNSL\QDPIN WLTQAEQTLNVASRPSLILDTVLFQIDEHKVFANEVNSHREQII ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVVQRLVERGR SLDDARKRAKQFHEAWSKLMSWLEESEKSLDSELEIANDPDKIK TQLAQHKEPQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD DMLSELRDKWDTICQKSVERQNKLEEA\LLFSGQFTDALQALID WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ ALKRSARELIEGSRDDSSWVKVQMQELSTRWETVCALSISKQTR LEAALRQAEEFHSVVHALLEWLAEAEQTLRFHGVLPDDEDALRT LIDQHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKHW ITIRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ WAETTLTDKDKEVIPQEIEEVKALIAEHQTFMEEMTRKQPDVDK VTKTYKRRAADPSSLQSHIPVLDRGRAGRKRFPASSLYPSGSQT QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRPFLGNQ PGDSQQLRLVRILRSTVMVRVGGGWMALDEPLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSAEGTPIQQSKLRLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR	
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDPSEDNRNKCRIATAPLIEAVENLTAFASNPEPVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TPVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAPQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLGVLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA EAMKGTEWVDPEDPTVIAETBLLGAAASIEAAAKKLEQLKPRAK PKQADETLDFESQILEAAKSIAAATSALVKSASAAQRELVAQGK VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE VERYREAIIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID MENMPDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR ETLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI RIDGQDISQVTQALRFRSHWELCPKDTVLFNDTIADNIRYGRVT AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA IKLVGEIKBTLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL DISKLAEFIIGMMGTLCAPARDEEVKKLKDIKEIVPLFRSIFSV LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV LLVTFSMAAPQIISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELBEVAI KFARLVNYNKMVPCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSANMIRDLSKMYPQTRHPAPHQPAQPFKPTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCPSCCSDGNI AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTKPDKYCLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKPTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MNGELTSPGAAVAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCPSCCSDGNI AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVIY
6034	2683	714	ESGRRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPEEAAAAM EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC RQIPKLLRQLQEPTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR LQFKVVDLEQTNLDEDGASALPDMIEYYESATHLNISFNKHIGT RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKFQRKGL VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSPIE TQKALLAEIQNGCKRNLVLARSREEKEQPPQLSASMPETTATEP QPDDEPAAGVQNGAPSPAPSPDSDSDSDGEEEEEEGEGERDET PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP PPGPEVKQQSCGLEHELSCSKNEKELEELLEASQESGQETL
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG YFYLMIPGFAILTKPLCKLTKENLADAIDPKSFSHSSPRSLKTA LENASTLALPDSSQPP\SLHTAEVQGCVVEILTQQLGPLPV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGCSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDSIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREPAEHIC\LL MEKGLINFMPKNRNLAVNIG2KK
6037	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPPEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHPI HNAEERRALAGARDLSADRPRLQHSPSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLQSPTLPDGTNNPP\AFSSQELASLPA PSMGLPGGGSPTTFLFRPMSESPHMPDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6038	1450	426	SSALQEFGTRNHTFGVPLPHRRKQTISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAAVAVSSPPSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLPAPY
6039	4073	1000	LDEYHARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPDAAELNPFQDPDSEEPITETASP RKTEDSFYNNSYNPFKSVQTPQYLNPFDEPEAPVTIKDSPPQST KKKNIRPVDMSKYLYADSSKTEEEELDESNPFYEPKSTPPPNNL VNPVQELETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSN RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA ETLELSDLYVSDKKKDMSPPPICEETDEQKLQTLDIGSNLEKEK LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER ARQLIAEARSGGKMSELPSYGERAAEKLKERSKASGDENDNIEI DTNREIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLE VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEQKQ IDTRAALVEKRLRYLMDTGRNTEEEEAMMQEWFMLVNKKNALIR RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE QLLLDELVALVNKRDALVRDLDAQEKQAEEEDEHLERTLEQNKG KMAKKEEKCVLQ
6040	475	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV GMIPDIYEKEVRLMIPL
6041	2	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS NLLQVLQKPKGSLKSSKKKNGKVRPADEILESNKENEKCVSSEG EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE IAKLVQKNPAVQFLYQKLIGNLNEDQRKDFGFLVDILYSALRCC DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPWL KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAPFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAE TAVEVPNKDPKTFPTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALNKNN VDKRFEGVEDCMICFSVIIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF
6042	1306	253	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDNEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAPL GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLNYWLTFHLVR
6043	403	599	LCLFFPFPCATPVLPLPSLYSAL7CLSHLSVSSWFCPCQPPLPC PLPPLQNKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRFQPPPPPPPG AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFPSSL SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVLLVIDEPHT DWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVL RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS VNSLHSVYNFCDKPWVPAQMVRLHKKLQTEEFPLIDQTFYPNHK EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT KTYATABPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA MLEQIAMSDRYKLWVDTCSEIPGGLDICAVEALHGKDGRDHIIE VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ ATRQTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ AGPVPTTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA AAGGPPHPQLNKSCSLTNAFNLPEPAPPRPSLSQDEVKAETIRS LRKSFASLFSD
6046	212	1075	EGLTG?CERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK QAPLSPGLPAMGGPGPGPCEDPAGAGGAGAGGSEPLVTVTVQCA FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF VVPAGPRMSGAPGRLPRSQGGDQP
6047	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD KGGRVVIFQREPESKNAPHSQGEYDVYSTPQSHEPEFDYLKDLE IEEKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN LKDEEGKLKDLSTVTSLQVPVLKPNDLMVEVSPRRIFANGHTYH INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA WNGSDSVIMTQA\YNNFFRMFDRNTKRDVTL\BASRESSKPRAV LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA TNNLYIFQDKVNSDMH
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD DGPSVNDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK SARPI/APLAIPPQQIYTPQTATPTAASPGSSSGLTATVAQAMP NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKDKKKKESSKE LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTQPLTPLHVV TQNGAEASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEQLVK EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP YGSKVSGGEDADKARASPSVTCKSSSESKALDILQQHASHYKSK SPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRT SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQQG STPSLYPPPRR
6049	215	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRMV NGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASL GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSP QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWYTS AASSINSHLPPPGSLQHPLALASGTLY
6050	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIPKEREEDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6051	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6052	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6053	201	1704	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPA HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD RFNLJLADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS
6054	1	1054	PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHP VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISQSAGPPPGTLQCSALHHDP GCANCSRFCRDCSPPACQCHTHVPPGNALNGVQPPELSRTLALI SSREPPRKKKKSQTETGKERERTSPLTQGGKRFELQHGLAGICM TLLITGDSIVSAEAVWDHVTMANRELAPKAGDVIKVLDASNKDW WWGQIDDEEGW?PASFVRLWVNHEDEVEEGPSDVQNGHLDPNSD CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKQC RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDPHL SEIGPCPLEHQDGPWIYSEYCNNHLDACMELSKLMKDSRYQHFF EACRLLQQMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAQDH SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWE GRDILDRSSELIYTGBMAWIYQP\YGRNQQRVFFLFDHQMVLCK KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDPNVSMKNAFKLH NKETEEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFEISE NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYLVP \DGIAQSQVFEFTEPKRSQSPPWQNFSRLTPFKK
6056	43	3358	SGGRGPVRVRSEQLSFSAEQVSQISQISLGRRFLSSLFPPPSRA LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPIQQ MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYEDL ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE EECGISIEGVNTPYLYPGMWKTTPAWHTEDMDLYSINYLHFGEP KSWYAIPPEHGKRLERLAQQFFPSSSQGCDAFLRHKMTLISPSV LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT VRWIDYGKVAKLCTCRKDMVKISMDIFVRKPQPDRYQLWKQGKD IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP KADEEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNTEA SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA YAYRSVPSISSEADDSIPLSTGYEKPEXSDPSELSWPKSPESCS SVAESNGVLTEGEESDVESHGNGLBPGEIPAVPSGERNSFKVPS IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF IYSEENIEYSPPNAPLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGWLCARCKRNANTAECCLCNLRGGALKQTKNNKWAHVMCA VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKNPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARP VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIP LSGTY
6057	1	853	FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRPVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIPG WGDFYSNIKTVALNLLVTGKIVDHGNGTPSVHFQHNATGQGNIS ISLVPPSKAVEPHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG
6058	1	986	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRHARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILABAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIPGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP
6059	2	3650	QQDFESLADLTDHRAHRCPGDGDDDFQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK EHLAKSEKEAKKDDFMCDYCEDTFSQTEELEKHVLTRHPQLSEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ADLQCIHCPEVPVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV \EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV ERGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS KKSKAEQSPVSSDVRVSSPKRQRLSASANSISNGEYPCNQCDLK FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH YMTTSTHYVCESCDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ VHVKHSHLGNPAKAHKCIFCGBTPSTEVELQCHITTHSKKYNCK FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAB PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMQTVT STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHECKLCNQM FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVPVQANKLQQHIFA VIGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
6060	2145	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVINSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYPTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIPRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEIAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPPPLCWCLREDDPQ
6061	110	1330	MNIHMKRKTIKNINTPENRMLMLDGMPAVRVKTBLLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHPQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDP\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV
6064	913	311	NLPQSLPRPTEHSPPYSLEKNTDLVAVWDVALSDGVHKIEFEHG TTSGKRVVYVDGKEEIRKEWMPKLVGKETFYVGAAKTKATINID AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV LEKDAMDVWCNGKKLETAGEPVDDGTETHFSIGTH\ACYIKAV\ SSG\KRKEGIIHTLIVDNREIPEIAS
6065	1153	641	MSVRVARVANVRGLGASYRRGASSFPVDPPGAQGVAELLRDATG AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR ELYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIPVASLAAV EKLHHLQPSVIENCVAAAGPSVGEFAALVFAGAMEFAEG
6066	68	3470	VKENMPATRKPMRYGHTEGHTEVCPDDSGSFIVTCGSDGDVRIW EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDQTCA ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR ESWSHQPDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDPLNDNAVEIP SPSKGIINDDEDDEDLMMASGRPRQRSHILSDDENSVDISMLKT GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTFRQKPPQS GSTPLHLTHRPMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHAT HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQKEVF SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELGKKKK QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP TLPRPAVAILSFKLPYCQIATEKGQMEEQPWRSVIFHNHLDYLA KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGQNSPSKSTNSSDVSAKSGAVTFSSQGRVNPPKVSAS SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI CPPQNTENQRPKTGPQMWLEENRGNILSDNPDPSDEADIIKEGM IRFRVLSTEERKVWANKAKGETASEQTEAKKRKRVVDESDETEN QEEKAKENLNLSKKQKPLDFSTNQKLSAFAPKQE
6067	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLP PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV SVDQKERCIIVRTTNKKYYKFSIPDLDRHQLPLDDALLSFA\T PTAP
6068	13	1730	GSKMADLANEEKPAIAPPVPVFQKDKGQQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW RSPSEAADEVCALEEKEPQKNESSNASEGEACEKKDPATQQAFV PGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA AAESGSESSSQEATPEKESLAESAAAYTKATARKCLLEKVEVIT GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG TLQSRLSDAGPRGSLR\LILNTKLNAQMQIDKASEK\SIRITAM DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS T
6069	583	27	PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN IDELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER RPALLCVLSCI
6070	478	858	IRVTVDGEPLHYIFFLQFLDSPEW/RFTETHRGRHF\QVTLTAE TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP ARLTLGRWERAPLASQGWKSRRARRDHPSIERAQQEAPAVRKLS SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS RQPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL QGQMPALMRVGIPQSFQKSSRDILLCTDIASRGLDSTGVELVVN YDFPPTLQDYIHRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI ELAARRRRSLPGLASSVKEPLPQAT
6072	1	742	KMERTEMMPTINSQLEPKSKPPPLVSSSRWLVKRGELTAYVEDT VLFSRRTSKQQVYPFLFNDVLIITKKKSEESYNVNDYSLRDQLL VESCDNEELNSSPGKNSSTMLYSRQSSASHLPTLTVLSNHANEK VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSPT AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT LVEAIKKVKDHRGIIPNRGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCNATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG VQPSVIILLSLFSTPHGAKSIIQEPPEITILTTEVHPVAPTHPG QKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTPETVFIPWGPPSKMQKPQGSLVRVIQRAGLVFP NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI QNEHSRKGNHHRFITEKRVFSSNAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTRAQVQLVQSGAEV KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEQEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLYISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS NGLICSGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQIC NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD VDDCWFYPTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY KSAVTTVVNPKYEGK
6078	1426	180	BTEDVMELLEEDLTCPICCSLPDDPRVLPCGHNFCKKCLEGILE GSVRNSLWRPVPFKCPTCRKKTPSYWELIPLQVNYSLKGIVEKY NKIKISPKNPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR GEHTKHVPCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK LAVMQAYDPEINKLNTILQEQRMAFNIABAFKDVSEPIVFLQQM QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTNFLEWSL FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE RFKNFTLVVLNNVAEPVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP GVLDRLYGHPATCLAVFRELPSLAKNWVMRNLFLEQPLPQAAVA LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIPRQ NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGPQFL LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLPQLSFSTLGKD YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL SSGVSGAGGTVHQPGPIV\VETNYRLYAYTESELQIALIALFSE MLYYFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHSDVKRFWKRQK HSS
6080	1	1199	IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKVLGQDFK TLRQQCLDSGVLFKDPEFPACPSALGYKDLGPGSPQTQGIIWKR PTBLCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV EGPEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY SAAEAEAITSQKLVKSHAYSVTGVEEVNFQGGHPEKLIRLRNPWG EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR QFSRLEICNLSPDSLGSEEVHKWNLVLFNGHWTRGSTAGGCQNY PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE TQGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP GAGVTTERTIQLSVSWKSQTVEEVVVLAVGVVAVKILLLCLCLI ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1288	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLLSRPPSAAMDGDGD PESVGQPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL LKCQQEGLVPEGGVEEERDHWQQPYPLSKRRNLLRNPCGEEDL EGWCDVEHGGDGWRVEELPGDSGVEPTHDESVKKYFASSFEWCR KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR FVRPEHGGQDSVYWKGWFGARVTN3SVWVEP
6083	1865	309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM VVSVTASTTQGQQLSEEELRRLEEACDMALELNASKHRIYEYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL RRKAARLVAAKCTLAARVDSPHESTEGKVGYELKDEIERKFDKW QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGPSLGHLGKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6084	1865	309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSVGEEEEEPAIE DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIN VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL RRKAARLVAAKCTLAARVDSPHESTEGKVGYELKDEIERKFDKW QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	SGFRSFQQNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEEEEEEDEDEEER KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFALR RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR VTGRLLTGDCQKNIHLWTPTDGGSWHVDQRPFVGHTRSVEDLQW SPTENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDVNV ISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVT SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGPTIFRT ISV
6086	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKPKYPP NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKIVVVLDSMIKV PTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG HVQLVDLASTEKPPVDIPAHEGVLSCIALNLQGTRIATASEKGT LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLICVSSDHG TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT DDKL
6087	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCENMPCTCTWRNWRQWIRP LVAVIYLVSIVVAVPLCVWELQKLEVGIHTKAWFIAGIFLLLTI PISLWVILQHLVIYTQPELQKPIIRILWMVPIYSLDSWIALKYP GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVLILEAKD QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK EELSPIQPVGKPLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEAEE GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP TTAKISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE LERQRLLRCPPPPVRRSEKPNWDYHAEIQAPGHRLQENFSLDLL KTAPVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTPFAVIGALLQSSGPERTALPIRDFLI TQMTGKELFEMWKIINPMGLLVEELKKRNVSAPESRLTRQSG\A

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEAARVALRKLYGP TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS PIKYGYQPRRNFWPARLATRLLKLRYLILQSAVGGGYTAKETPD QWKDMIPDLSEYKWIVPDIVWEIDEYIDPEKIRKALPSSEDLVK LAPDFDKIVESLSLLKDPFTSGSPEETAFRATDRGSESDKHFRK VSDKEKIDQLQSELLHTQLKYQRILERLEKENKELRKLVLQKDD KGIPPIESLRKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVG DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIPVLTKVDL AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI REYEEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES VEQQADSFKATRFNLETENKNNYPRLRELDRNELPEKAKNEILD EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSG TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE SRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV KEVLEDFAEDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE ALHQEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLAIQTVVPLQHCKIPELPVQASYL FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRPTV LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR P\RKTSLFNHMASMGPRBAVSGLAKSRDYLLTLR\RRGSSTQDS CMARTPCP/PIACCLSPSLIRSEVEPLKMDFNWRMKEVLVSSML SAYYVAPVPVWPVKNTHYYDKRWSCELFLLVSISTSVILMQHLL PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEEDWWPQGV LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS
6091	3279	412	SSRTREMEEKEILRRQIRLLQQLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVQSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQARBASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SPRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRPGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLDSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
6092	143	3190	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLYLCNKTAVQ EVFKPENISLRNKLRELCVKLMPLHPVDYGRKAEELLWRKVYYE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VIQLIKTNKKHIHSRSTLECAVRTHLVAGIGFYQHLLLYIQSHY QLELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY LGDLSRYQNELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL LIFQMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE PASEEGSESESGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNP DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\ PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV IKD
6094	23	1010	PPLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR FYIKCTRCLAEITPKTDPENTDYTMEHGATRNFQAEKLLEEEEK RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR QAHVDFEAMLRQHRLSEEERRRQQQEEDEQETAALLEEARKRRL LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG GQPYTPDAWRVLPEPTGCIPGQ
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ YTIRCRPLQFQPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VKVHTVPKPGKGADLSKPPCRKAKETRKERKRLKLMQQNPAQSL EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVIDILPN CVSSVYLYYDPDYSPLSLGVYSALREIAFTRQLHEKTSQLSYYY MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSLENSK YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS EEAAVLQYASLVGQKCSERMLLFRN
6096	2277	575	QRVRAALLSSAMEDSEALGFEHMGLDPRLLQAVTDLGWSRPTLY QEKAIPLALEGKDLLARARTGSGKTAAYAIPMLQLLLHRKATGP VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAA EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVV DEADLLFSFGFEEELKSLLCHLPRIYQAFLMSATFNEDVQALKE LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK LSLIRGKSLLFVNTLERSYRLRLLFLEQFSIPTCVLNGELPLRSR CHIISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDP EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV LTPVLPTEQFHLGKIEELLSGENRGPILLPYQFRMEEIEGFRYR CRDAMRSVTKQAIREARLKEIKEELLHSEKLKTYFEDNPR\DLQ LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL PLVGRPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLMS
6097	1673	192	APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPQPPTGPP PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRPRVVKLPHGLGEP YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSPTGGLGQ LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPLPSL RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLDS RPSSPALYFTHDASLVHKSPDPPGAVAAQKFSLAHSMLAISGHL DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPPA PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVPPGVG VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPPGEET QPPPSLPGTPQQ
6098	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD EGKIPKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDPEYTAKIRTLAETERPF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAPGRSFGKD
6099	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD EGKIPKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDPEYTAKIRTLAETERPF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAPGRSFGKD
6100	2	713	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSIGTSVGP SASQRNSRDIGSNSGCC
6101	1	1399	PRGRAWPLRRVSHWLGCRRVCSWSASWGRLFALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE AMPLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNABES KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER HLAYLKWISQIEELSDNIQQYLMTNNVPEAASTLVSMAELDIKL QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWFFIA PPQSQTVGLSRPASAPEIYSYLETLPCQLLKLQTSHELLTEPK\ HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLQFLE LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA DWADNVPFLQLQQAALEVPAENNTLSKLQLGQLASMESSVFDDM INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFWQMLVEKLD VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT	
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWFSSRLEATRMVVPVA ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD QEAAAILMARLAIYRABTEEGPDVLRWLDRQLIRLCQKPGEYHK DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES GAPILTDDVSLQVFMDHLKKLAVSSAA	
6104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR CNLLYSKDTEPGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQVQPSEVGRPEVTPPGPGAP
6106	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIKSRGRPAAS AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPQG WSRARHCPGGLCLLLLLLCQFMEDRSAQAGNCWLRQAKNGRCQV LYKTELSKEECCGTGRLSTSWTEEDVNDNTLPKWMIFNGGAPNC IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGS STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYS\SAC HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEAACSSGV LLEVKHSGSCNSISEDTEEEEEDEDQDYSFPISSILEW	
6107	623	168	SRCSSPRPEPGRGRGK/LSPSEHRKWVEVFKACDEDHKGYLSRE DFKTAVVMLPGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK KKEAQRYRNBVRHIPTAPDTYYRGFLTLEDFKKAFRQVAPKLPE RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVPVVMCCSMLVLL YYFYDLLVYVVIGIPCLASATGLYSCLAPCVRRLP\SASAGESA LLAPTIPNNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ WAWVLQDALGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL ALCDRPFSLLGPGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI AYGVGLLVTFVALALMQRGQPALLYLVPCTLVTSCAVALWRREL GVFWTGSGFAKVLPPSPWAPAPADGPQPPKDSATPLSPQPPSEE PATSPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGRDQAQPS PVTQPGASA
6109	1	1381	CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQRVSEFP MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQIYDLVD RHLRKLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAPKNNDFQLOKEP SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKNNNKSSS QQSSSSSSSSSLSSGSSSSTVVQEISQQTTVVPESDSNSQVDWT YDPNEPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATWSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGGIAVSQ ARSSSTGSSSSTGGGGOESQPSPLALLAATCSRIESPNENSNNS QGPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG SSTNGSNGSESSSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP NIQYQVIPQFQTVDGQQLQFAATGAQVQQDGSGQIQIIPGANQQ IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNPTTSG SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKEGE Q\NQQTQAAPKSLSRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA ISQETLQNLQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQLQNLQ VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIPAGTVT VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH GAQLGLHGAGGDGIHDDTAGGEEGENSPDAQPQAGRRTRREACT CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK RFMRSDHLSKHIRTHQNKKGGPGVALSVGTLPLDSGAGSEGSGT ATPSALITTNMVAMEAICPEGIARLANSGINVKEGGQPCSPINT SANGF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6111	1637	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG SVEAVARLKRSRLKVRFCTNESQKSRAELVGQLQRLGFDISEQE VTAPAPAACQILKERGLRPYLLIHRDGV\ASEFDQIDTS/STPNC VVIADAGESFSYQNMNNAFQVLMELEKPVLISLGKGRYYKETSG LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHQ AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDEHHPEVKADG YVDNLAEAVDLLLQHADK
6112	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK
6113	1779	567	WEGRSWAACGVNLQGAWGERSGVRASEAESPGKRADVSWWSRQL ETMVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVL TKECRKKAKPRIPFLFNDILVYGSIVLNKRKYRSQHIIPLEEVT LELLPETLQAKNRWMIKTAKKSFVVSAASATERQEWISHIEECV RRQLRATGRPA\STEHAAPWIPDKATDICMRCTQTRFSALTRRH HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRELAAQQRK EEAEEQGAGVPRAASHLARPICGRPVEMTMTPTRTRRAAGTATG PAAWSSTPRGWPGLPSTADPRPAEHLSPSQLHCPGPQEGSSRSC PGLRDPIPWWQVQRWGVALSGLPVPPCWTLCPYGPTAGNAFPFR KPQNTHRSW
6114	818	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAEQVQC GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSQVT GRPQWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
6116	595	1430	TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKEEEDESYTPVQ AARPQTLNRPGQELFRQLFRQLRYHESSGPLETLSRLRELCRWW LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL ASPLRSSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN LYRDVMLENYRNMASLGK
6117	1433	222	VGVPSPAPPCSWEVGPGGGWTPGILKEGQGGRRTPLLLLATRTR GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEEIQQQIWIPSVFIGERSSEYLRALFVYYEKGARVLLVPDN TFPLGYYLIPPTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK \EQLKQI\PTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDE GEPRDHPASERTPLLQSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV
6118	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEPLRIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II
6119	1217	462	DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNFSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKSPVBAVR VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE ILELAGNAARDNKKTRIIPRHLQLAIRNDBELNKLLGKVTIAQG G\VLPNIQAVLLPKKTBSQKDEGANDP
6121	1612	107	FVRAQARGSRQPVRRPLLGAGSRLRCRSCGRMEPLKVEKPATAN RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS VRLLGRVVFKLMDGAPSESKKLYSFYDLESNINKLTEDKKEGLR QLVMTFQHPMREEIQDASQLPPAFDLPEAFAKVICNSFTICNAE MQEVGVGLYPSISLLNHSCDPNCSIVFNQPHLLLRAVRDIEVGE ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL PDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIPFPG SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH SLIEDLILLLE/AMRRQHQSILRERSQRBIRRVSLLNALLRSHT LCFVSCVNLSYWKFCSVFV
6122	2	2324	RFRKMADGGAASQDESSAAAAAAADSRMNNPSETSKPSMESGDG NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA GGQITGLTLTPAQQQLLLQQAQAQAQLLAAAVQQHSASQQHSAA GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKRIDTPS LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND FSPTTIFRFEALNLSPKNMCKLKPLLZKWLNDAENLSSDSSLSS PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSPLEN\QKPTS EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSSA SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA PNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASAGNSAPVASLHA TSTSAESIQNSLPTVASASGAAASTTTTASKAQ
6123	3	2944	HLLHRWFGTDMQMINFTTGEFQLTEACPVLGTHSEESRFGILHL HLQFLEMKRVGVVPTPADYGKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEEGPWRLTVPPVSLSLLGVILIAFQQAQYILM EPMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DXGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HXTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVPSNPSSBCS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPPVEQEDPYRKKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDPERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTQVEEDKGLYSPGDLWPTPPVCVTSSLNCTLB NGVPCVIQESAPVHNSFIDWSATCEGQPSSAYCPLELNDYNAPP EENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A NRNANFPLSRDSSYCGNV
6124	1573	236	SDEALRLAGERGMGRVQLPEISLSHGRVVVSPGEPLAGTVRVRL GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF SKDHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKTG SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPQSAL PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPCPSEPPA RPGAASWGPTPGG\PSAPPQEEAEAAAAGGPHPLDPVFLSTKS HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVE PSLTPES
6125	1	904	KTCPKLTCAPTVSVPDSCCRVCRGDGELSNEHSDGDIFRQPANR EARHSYHRSHYDPPPSRQAGGLSRFFGARSHRGALMDSQQASGT IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEBL PGQSFDNKGYPCGEETMPVYESVFMEDGETTRKIALETERPPQV EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI PTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
6126	1224	389	RLLSEAPCPRSRRRFQMNPEWGQAPVHVAVAGGLCAVAVFTGIF DSVSVQVGYEHYAEAPVAGLPAFLAMPFNSLVNMAYTLLGLSWL ERGGAMGLGPRYLKDVPAAMALLYGPVQWLRLWTQWRRAAVLDQ WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH FQGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQPHFAFLFL THFNTHPRFHPSGGKTR
6127	1335	463	VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRPDADEKGV IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQIWRKYDA DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR NKDGRLDLNDLARILALQENFLLQFKMDACSTEKRKGDFEKIFA YYDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKFREILL RHCDVNKDGKIQKSELALCLGLKINP
6128	2511	843	TCRMSRRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD SPGSLDGRAWEDAQKPQSANCGGRKTRVYATSSRRAPPSEGTRR GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP TRCLPGHKEEEDGEGAGPGEQGGGKLVLSSLPKRLCLVCGDVAS GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKAC QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGLGELG\ AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS SCEKLLHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAG KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD
6129	1764	771	ARFARSAHEGKMPKKKTGARKKAENRRERERKQLRASRSTIDLAK HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLIDAEC\VECERGVNDHGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETFKCVSCNRLGQHSCLRCKACPCDDHTRSKVFKQEKG KQPPCPKCGHSTQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSSDKYGDTSYHDEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEQEN
6130	3	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DFVRKEIEV\DSSPSVAGISWTQQGTEQP\ASMRDLYIKKGQGC ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\LVGN\SVD LESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRQ MNYAAQPDKDDPCCSACNIQ
6131	3	1811	SSPREKTSDSSERPSRHGPLFLRLVGLSPPSVLCVPPSRPVPGS PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLVLGGCLGVP GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTPS SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWQKI QEPNTFPAILRSMCGYQTFP\AGKYLNEYGAPDAGGLEHVPLGW SYWYALEKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVSL DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQNVFAPRN KNFNIHGTNKHWLIRQAKTPMTNSSIQPLDNAFRKRWQTLLSVD DLVEKLVKRLEFTGELNNTYIPYTSDNGYHTGQPSLPIDKRQLY EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLG PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEPDDQEVPV EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQQPPFALSRPLPSCVESGW AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD FKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL PQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVPDELFKLAPEKVNA VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	PVHGSMADTDLPMECEEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATCPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPQPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRPMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPPQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTPRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALPKNSVSGIKLACTSCTPVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEQAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLPL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DVCIKRTVKNFLHKKWKEQARE MADTACDSDVLLQLVLVWLGEV LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6134	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASPVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPSELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQRBQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL DVCIKRTVXNFLHKKWKEQARE MADTACDSDVLLQLVLVWLGEV LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6135	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASPVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKNSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPSELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQRBQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL DVCIKRTVKNFLHKKWKEQARE MADTACDSDVLLQLVLVWLGEV LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6136	1704	539	PGVRMALEGMSKRKRKRSVQEGENPDDGVKGSPPEDYRLGQVAS SLFRGEHHSRGGTGRLASLFSSLEPQIQFVYVPVPK\ESALASA DLEEEIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIQ INQEEERLKNERTVPVGNLPVTCNKKKLKSFFKEYGQIESVRFR SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK RNGAQIADGFRIRVDLASSTSSRDKRSVFVGNLPYKVEESAIEK HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPHERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPPAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFPQEEEMYRVDIYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVPQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLFRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFPITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRPGQPHLALSGGSSPVALPQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDGGAHIYARESALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSKVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG
6138	4587	934	EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHPQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSNKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELNEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEENIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAPI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAE RTAACPNSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRRLRHFT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NQREEFEGTRESILVWLTEMDLQLTNVEHFSESDADDKMRQLNG FQQEITLNTNKIDQLIVPGEQLIQKSEP\LDAVLIEDELEELHR YCQEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE WDHTGRRGGPSSSH\EEDEEAQYY\SALSGKSISDGHSWHVPDS PSCPEHHYKQMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLACLL PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
6139	52	1131	LGDNVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN TQRFLSQHRCGEPEASPPRTLSDLLLASMVAGVVSVGLGGPVDL IKIRLQMQTPPVSGRQPRFEVQGSGSCG\EPAYQGPVHCITTIV RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV LDCISQSYQKEGLKVFFRGITVNAVRGFPNSAAMFLGYELSLQA IRGDHAVTSP
6140	694	136	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRRTDVRITG
6141	2	904	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGPSSIQELYAQIAGAFEIS PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKKEELPTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAPP DEFVFDVWGVIGDAKRRGL
6142	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP
6143	2802	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTIGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVNTEKSPFTTPIGRKDEADLAKSALAMADSDHL TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LIKLVKAAGFSSSTTSTSWEGNRASQTLSVQEIALLKAVLVAGL YDNVGKIIYTKSVDVTSKLACIVETAQGKAQVHPSSVNRDLQTH GWLLYQEKIRYARVYLRETTLITPFPVLLPGGDIEVQHRERLLS IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI LQIITELIKTENN
6144	1289	568	SGPGSMSGGRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPVQN VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS VGDRTVTIGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV \VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPQD /TKAWLKEHVEPVP\GPP\QFVRF\SWRTAQTI\LEKEAEDVIR EDSASENQEGLRKITSYFLNEGSQARPRSSIRYFLERGLESTTS L
6146	428	781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS R/YPGHEAHDQGG\WDARQSIIRKVVJPETGRTRLIKGDGEVLE EIVTKERHREINKQATRGDCLAPQMRAGLLP
6147	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDPRKME DEMDRLATNMAVITDPSARISATLQDRHERITKLAGVHALLRKL QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S SGFVGGLCQVAAAYQELPAAQGPAGAEKLAAFARQLGSRYYFALV ERRLAQEQGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGBF CSQGVREGLIVGFVHSMCQTAQSPCDSPGBKGGATPPALLLLLS RLCLDYETATISYILTLTDEQPLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDNLSTLEPRNVRAVMKRV VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIVSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNNWEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDQ ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PVAEVLDTEGSIQNFFRKVAPSENGPNGISAEVMDTYVKSCAGY CVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPP MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANPIKNGKTSPASKDQRTGKKTSVQGQVQKGND ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ PQQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\LSWHPP\HQGL S\DIRADHNT\VLPGR\PRQNSLHGSPHSADVLKMDDFGAVP/F LTELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKQ
6150	372	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEPDWNDGNG QEGWPPMDQSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAPG QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG KIYYYHVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPTYDEN PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DLEC NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS GKTDSRERKSCQPFCSTPVSTVLLMIHHPGEFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM NGEPLAAEKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLLICFNVGSGLHLQVLSTRNENKLLPKH PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDRETPFFLLTG YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVPDADEIGSDN WLANFTFASGNEGGYFHIITDAQTNEGIVTLIKEVDYEEMKNLD FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP AAIALMILAFLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP WNNEGAPPEDKVVPSPLPVDQGGSLVGRNGVGGMAKEATMKGSS SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNYAVQQNVTVTERVL APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGANFKPTISDKSHLLQHVSKLDLTDAKN SDTAHIKSIBITSILNGLQASESSAEDSEQBDERGAQDMDNNGK EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDBD EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVAEKRIKLL NNSDERLQNSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA SPPHPADPEEGVAEESLQTVAEEESCSPSVBLEKPPPVNVDSKPI EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS RQQSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS ERS*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK FIKKAEKKP*SNSGKQQKEGK
6155	869	121	HLLPELR3KSWITWKYVFYLGVLAGTFFFADSSVQKEDPAPYLV YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG TEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN P\PTTNVRPGTVCLLSGLDWSQBNSGRHPDLRQNLEAPVMSDRB CQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE VGHFMGGDVGIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAPGKLLKSIPLGV FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ DVSQWTTADNDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN ALTSPPKVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLAGQPAVT VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS PEVINYLGNKACECVISTADWAAVQEWQNAIHDLKKSTSSTSLN LKADFNYIKSLSSFESGKFVRCTEQLELLPGENINLLAQGSKEK IDMKKLLRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDYEH PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK QMEQISQFLKAABTYGVRTTDIFQTVDLMEGKDMAAVQRTLMAL GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVFILAQNPGLAQN PILEGKDHNQNTGVDPIIDHVQDRKTD/SRSKSPHKRGKSRER RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKERERERERERKE KERGKNKDRDKRRKDREKDKEKDRERERERERERKEHEKDRDKEKEKE QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE RRRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD HISERRERERSTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHPGHPAIM NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGQR IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF DVSVSCDCTTAYQPG
6160	1626	1790	AGAKFPP*P*KVADAQPTESEKEIVNQVNVVLKDAEGILEDLQS YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKPYEPSQR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEAALRGLLGALTSTPYSPTQHLEREQALAKQPAEILHFTLRPD ELKMTNPAIQNDPSYYRRTLSRMRINNVPAEGENEVNNELANRM SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLSTMASVC RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI KSMLQ*QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEJGISH*LLEKH* KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISSDS TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPEIVYS GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFGHWTVE CTGKRKYLHRPSRTAELKKALKEKENRLLLQQSIGETNVERKAK KKRSKSVTSSSSSSSDSSASDSSSESEETSTSSSSEDSDTDESS SSSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAPTYKFFL TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIELIRQR ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFPEGSEIIL RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE LMQTVYSMAPFPFPQLAELREKYTYNITPPPATVKPTSVSGRHS KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN GGERFG
6165	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFPEGSEIIL RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE LMQTVYSMAPFPFPQLAELREKYTYNITPPPATVKPTSVSGRHS KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK LDLPREAFEAASREDFELQGYAFEAAEEQLRRPRIVHVGLVQNR IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICPQEAWTMP FAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDPNESTYYM EGNLGHPVFQTQFGRIAVNICYGRHHPLMWLMYSINGAEIIFNP SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL NLCQQVNDVWNFKMTGRYEMYARELAAEAVKSNYSPTIVKE*PAS VPALG
6167	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ VQRCEDILQQLQAVVPQIDMEGDRNINIVKPGAKSRGRGIMCMD HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK*APLYLTPEGWS LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG DRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDGKWV VQKYIERPLLIPGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST QPFSLKNLDK
6168	84	1392	VWPVPSVSAMPFKKQAQAGGSKKAEQKKKEKYIEDKTFGLKNKK GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL PPGFVLKKKKKKKKEDEISL*DLIERERGALGPNVTKITLESF LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRDVD ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN EREGTENGAIDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAEPEEDLNLPNAVITRIIKEALPDGVNISKEARSAISR AASVPVLVATSCANNPAMKGKRKTLNASDVLSAMEEMEPQRFVT PLKEALEAYRREQKGKKEASEQKKKDKDKKTDDEEQDKSRDEDN DEDEERLEEEEQNEEEEVDN*KGRETVAPWKVPLEMRRATCFCE AFPCWAE
6170	62	667	STKVMLPNTGRLAGCTVFITGARGIGKAIALKAAKDGANIVIA AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGRLAESQGT NATLRYTKSK
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALAIQGSLEFDDAGGEGV TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLF FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF LSTE*AAPRPLGQLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAPVQ HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI LDHIRERSQGPSLGP*H*WPSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRANAAPVKGNRKQSTEG DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ AFLVSLYKPMKERHTPIERVPHLGFKQINLMKIYKAVEKLGAYE LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG SLREEAQAGPCPAAPIFKGCPYTHPTZVLKPVSQHPRDFFSRLK DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP KPKACWVSPNAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLIGPALGPVPPEA YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIGASGFSBSSLFCKWGIHTGAAWKLLS GVREGQTQVDTPQIGDMAYNSHPIDLHFATKGLQGWPRLHFQVW SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPQTSGCSDRPP VCPI
6178	1027	254	STQRGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL HCHSNFSKKFSFYRHHVNPKSWWVGDIPVSGALLTDWSDDTMKE LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL P?PKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHPNRHGK FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFPGI
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECQN* SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GNHIKSYVLGVKGADYRDSGDLVHHWVQNVLSEPVMSEIRTVYV TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE LSN3SQPTLQLVLPTYVRLEKLPTAKANDAGTVSKLCHLFLBAL KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN NCEQALLIKRRRLLSPEDMNKLMFLKSNML
6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRVRKNAYLPI YYLIQPCGHSWIFTNMTVRPFSPGKDSMVDTFYAIGLVMRLCQS VSLLELLHIYVGIBSNHLLPRFLQLTERIIILFVVITSQEEVQE KYVVCVLPVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLMMP IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR KDRLWIQCSK*NTGSILVEKPLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI VRPFGSSVNTPGKLGCDLDMPLDLDETRNLSAHKISGNFLMEPQ VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR PSHQASGPQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR CWARAHSLTSSIPGAWITNFSLTMMVIFFLQRRSPPILPTLDSL KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS APNRKSFTKKKSNKPAIETVKNLLESLKGNRTENFTKTSGKRTI STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC GSGCGGCGSSCGGCGSGCGGCGSGRGGCGSGCGGCSSSCGGCGS RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC CQSSCCKPCCCQSNCCVPVCCQCKI*QSGPRPSGFSCLVKAFLM VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGGARGAEE EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHENNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLPQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDPVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLMPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEEELQQNLWGLKI NMEEESESZSEQSMDSEEPDSRGGSPQMDDIKVPQNEVLQTLQR GKEENISCDNLVLEINSLKYAYNISLKEVWQVLSHVVLEPPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLBALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSSEDD
6185	791	44	PCTSCVLWATLHLFASTRKAPQAECGNISITTEWQKIGVGYTGVG IFFILFGTLLYPDSVLLAPGNLLPLTGLSLIIGLRKTFWPFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFPPVAP GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK
6186	569	238	VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KERKVKNKVKNKADTEEVPNNSPTNQEKMPTSAILPDFSGSVIS NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQQI PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE EPENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELEAFNMLK VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA VIALKKQQ*TPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP PSGSRVGSRYD
6187	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSIWVQAKSVKMDV GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA A
6188	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW NIGVPICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD INAFRKEKDDKWKRGSEPVPEKKLEPVVPEKVKMPQKKEDPQLP RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM AGMNFYGANGMMNYGQSMSGGNEQAANQTLSPQMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNELAALAR GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ LTRIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE EEBEDEVEEEETR
6190	66	1309	ILVGNVSFLLSPAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS TSENSTSALADVSWTQPNIIILTVIIIVVVLLMGFVGAVYMYRE YQNRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFFHLTPQQPKCPS MIDWIKKINYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM QDYMPSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ
6195	736	235	VANGLQSNMPKFYCDVCDTYLTHDSPSVRKTHCSGRKHKENVKD YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
6196	1512	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH QRLLMGLMVSELKDHFLRHLQQVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSAVLHFNSRGSAAEFAVPHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLKREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW
6198	111	1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTTLGNNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDBAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEDTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPGPTYSEWMBBKIEDDFDLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGPGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE
6199	144	1211	MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGD VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF HAL*
6200	702	96	LPEVDHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS QGLETFAKAQTGPLRSSLEESPPEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQRSAEYAEA RKRILGSAS?EEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP DGSQGFKQRR
6202	2	426	TNADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISQ DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAPASQHPA TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGER LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTA RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV PILSEEELSLLDEFYKLVDPERDMSLRLNEQYEHASIHLWDLLE GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA SAPAVEDQVPEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFTS GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVP PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMFQM NTQQVN
6204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC ANCKSPIQKNEGCN!MQCAKCKYDFCWICLEEWKKHSFVHWEVI YRCTRYEVIQHVEEQSKEMTVEAEKKHKRPQELDRFMHYYTRFK NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL AQKVNRPYLRTPRHKIIKAACLVQQKRQSFLASVARGVAPADSP EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRRHRQRRRGDVHS LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQHPQAW
6205	1	1200	RAHRGKMALEVGDMEDGQLSDSDSDNTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPEPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD LDKELDEYMHGGKKMGSKEEENGQGHLKRKRPVKDRLGNRPEMN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRTIGNKKA IELLMETAEVEQNGGLPIMNGSRRRTPGGVFLNLLKNTPSISEE QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD LDIP
6206	10	1442	IISERRERSCLFLVCIRCSCDVVEMGSVLGLCSHASNIPCLCGS APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMPYLLLSLLM IKVKSSSDPRAAVHNGFWPFKFAAAIAIIIGAFFIPEGTFTTVW FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEPVP GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRPGILSNCN HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6208	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEPVP GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRPGILSNCN HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6209	1758	829	ERLCPPCMQSKIYSYNSPNKCSGNRFPLQEENSVTHHEVKCQGK PLAGIYRKREEKRNAGNAVRSAMKSEEQKIKDARKGPLVPPPNQ KSEAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK TQQNRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM KIDLIDGKGRGVIATKQPSRGDFVVEYHGDLIEITDAKKREALY AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH
6210	3761	387	IPGMSKLRMVLLEDSGSADPRRHPVNLSPFTITVVLLLSACPVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDIIVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDLMNSSGGHSEPH
6211	3761	387	IFGMSKLRMVLLEDSGSADFRHHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSNDLDDAQV VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDLMNSSGGHSEPH
6212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIPELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGSGNPTRK
6213	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SXLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VIPELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGSGNPTRK
6214	2	460	HELAPSAIRRAARLGLGPARWQSRAAAFYPVRGFRTGWSFVGNV VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKRFSAYN YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRRQVH IGQLYSTDKLIIENRDMPRT
6215	2	1849	FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISHFHLDH CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAVDKKGE ANFPTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAGHVLGA AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST YATTIRDSKRCRERDPLKKVIHSTVERGGKVLIPVFALGRAQELC ILLETFWERMNLKVPIYYFSTGLTEKANHYYKLFIPWTNQKIRKT FVQRNMFEPKHIKAFDRAFADNPGPMVVFATPGMLHAGQSIQIF RKWAGNEKNMVIMPGYCVQGTVGHKILSGGQRKLEMEGRQVLEVK MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKMEFLKQ KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQGL LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHQLRPTC RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL LQAAAPSEDPGTKVLLVSWTYQDEELGSPLTSLLKKGLPQAPS
6216	11	393	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRRGEEGHDPKEPEQ LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGRGGGSGNFMGRGGNFGGGGNFGRGGNFGGRGGYGGGG GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYG NQGGGYGGGGGYDGYNEGGNFGGGNYGGGGNYNDFGNYSQQQQS NYGPMKGGSFGGRSSGSPYGGGYGSGGGSGGYGSRRF
6218	1305	906	SCERRGFIMADDLKRFLYKKLPSVEGLHAYVVSDRDGVPVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS
6219	2	890	AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLPEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
6220	227	764	EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLYEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMPRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH
6221	98	916	RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRARRLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITPVVYENVSHFL LDLREKRK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6222	2	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG PRRNPAWSLQAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH EFQAETKKLLDIVARSLYSEKEVPIRELISNASDALEKLRHKLV SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNLGTIA RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR SAAPGSLGYQWLSDGSGVFEIABASGVRTGTKIIIHLKSDCKEF SSEARVRDVVTKYSNFVSPPLYLNGRRMNTLQAIWMMDPKDVRE WQHEEPYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE CLSEKETEELMAWNRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRAS EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH
6223	3	715	DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGCY RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNED GQPDLGKARDYYTRACDGGYTSSCFNLSAMFLQGAPGFPKDMDL ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA QQVHKEQQKGVQPLTFG
6224	1	133	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHEK
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDPT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPELIRRLEQ GEVPWGEERRRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLXAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSPSVKGSLLRHQRTHSGEKPFVCKDCERSPSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS
6226	29	266	TKVSELLGGSQRLPFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6227	2581	890	MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGPGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIPVKDVPNSQLRHIRLENNENKPVTNSRD TQEVPLEKAKQVLKIIASYKHTTSIFDDFSHYEKRQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6228	47	1978	GRRCRRRGAVMELAQEARELGCWAVBEMGVPVAARAPESTLRRL CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV DVTPGSLTSAALGLEPVVLRDVRTACTLRAQPLQNLLLPQAKRG SLPTPHDDHPGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER EABIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGN RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQBKQ QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE ELCQGLSLPQWRLRWVQAQGALQKLCS
6229	1571	560	GPSLLGTRGTPNPARTLQIFFLYIGRRLTGRMAAVDDLQFEEFQ NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL LPIPGKNFVRLYIRSNPDLYGPFNICATLVFAIAISGNLSNFLI HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK VMNIVSYSPLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS VGAPVYMAAVIEYLAABILELAGNAARDNKKARIAPRHILLAVA NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILGP PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP TTAEIDLKEDIGKALEKAQGKSFLETVKELRKSQGPLEVAEAAV SQSSGLAAKFVIHCHIPQWGSDKCEEQLEETIKNCLSAAEDKKL KSVAFPPFPSGRNCFPKQTAAQVTLKAISAIIFDDSSASSLKNVY FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAVGGLQSLQSSLYSEEQ LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK AGKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL PEEQLTSCGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL AVLMIAAFLQPIRDVQRESE
6232	3679	1476	FVAGTTMAGPWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKRVL YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIARERIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSPGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPILSVSVDGT QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV TZDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
6233	1	2654	HSTRENLNAGNPNFPSEGHLVRSTGPGGSFAKHNVAQCVSPKGP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LACSRTYFFGATHVPVLGGDSKLPKKTEQIRLLSQIYAAVIEAV LAGIACYAKTSSLTKAKEVAEQTLGSGLDSFELIPFKAALRSKM TFHIHAVNNQGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLQSWP EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISPYDGDSTSTVA ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYQAFYSEVF SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAQKLFSALSQPAG EKRSSLKLLSAKLPELDWFLQHFAISSISQEPVMRTHLPVLLQQ AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW MVYRQIMDSSECPHAAHFQRYLSSALEAQQNRSARQSAYIRKKT RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEQRHPLLVQLQSL IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYL MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIQS SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA KQKPQRKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTQFV NPFGDKTDFHPLMDQFWNDYVEEANREIEKYNQSLEQQEYHDLF ELKP
6234	1731	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL DKQSDIQNLNEERILALQLCGWIKKGTDVDVGPFLNSLVQEGEW ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG LTKDGVDLMESYVDRTGDVQTASYCMLQGSPLDVLKDERVQYWI ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWPTWCHN CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV QP
6235	1	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPQ DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATQ IVMGGVTGWCAGFLPQKVGKLAATAVGGGFLLLQIASHSGYVQI DWKRVEKDVNKAKRQIKKRANKAAPEINNLIESATEPIKQNIVI SSGFVGGFLLGLAS
6236	1	703	WDQNKGAAAGGGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQXGNMEVARIHAE NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV
6237	312	720	PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK
6238	2	4666	EEVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWPLEESNETEKIAPTTELVP KGBMIKMNIDSIPIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMPGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEEENYKVPEYKTVISPHSKDQLNITLSKCG LVNLNNLVKAPTEAATGSSADFVKDLAPFMILNSLGLTISVSPS DSPSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHPNAMTSLSSK LPFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DTVEGSKKVTIRSPVQIRNHFSVPLSVVEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFSEIIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLNPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSPTCVTEMEKTDLDIAVIMT YNTGQTVVAPHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSXYHISVAEEGND KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFLLINHTK NELVQYNQSSLSEIEDSLPPGKAVPYTWADPVGSRRLKWRCRKS HGEVTQKDDMMMPIDLGEKTIYLVSFFEQLQRIILFTEDPRVPK VTYESEKAELAEQEIAVALQDVQISLVNNYTKQEVAYIGITSSD VVWETKPKKKARWKPNSVKHTEKLEREPKEYTESSPSEDKVIQL DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE AEVTENTEVELPHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLLKSIGATLTD VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL GLDVLGNPPGLIREPSEGVEAFPYEPYQGAIQGPEEFVEGMALG LKALVGGAVGGLAGAASKITGAMAKGVAANTMDEDYQQKRREAM NKQPAGFREGITRGGKGLVSGPVSGITGIVTKPIKGAQKGGAAG FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDESDLNH
6239	2108	634	XPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVVVL SLLEMSKFYSQLIVRGVLGLGVIPGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKESNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS
6240	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSYHF DPLSSGSRSSSLKSAQGTGPELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCTT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FPSKL
6242	198	1310	QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE SSEDIDQMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSV GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLQ NQHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPPADP VLDLPLPPPPPEPLSQEEIEAQAKADKIKLALEKLKEAKVKKLV VKVHMNDNSTKSLMVDERQLARDVLDNLPEKTHCDCNVDWCLYE IYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVP KNPQNFYLDNRGKKESKETNEKMNAKNKESLLEVRLILQSGRKE KDVCSIFKSFASENNGKI
6243	1509	614	RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTRRATCRSA AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVRTGPPAH SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
6244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTWSLWSWVNQPSELSK FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
6245	81	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW KGEVKKRLDSEYKEGGQRNWVQVPCNGAVPTELALLYMIENGPG EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYPLTQLIFV NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG
6246	1177	359	SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS
6247	3	1678	NSRVWGPWTEPSAGSLRPNARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLAANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLPGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAPQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP
6248	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLRRIQQFSQGGTRKS ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPPRKDLEKYKDLDEDELLGNLSETELKQLETVLDD LDPENALLPAGPRQKNQTSKSTTGPFDRSHLLSYLEKEALEHKD REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA SDTELCDLAAILGMKNLITNTKFCNIMGSSNGVDQEHFSNVVKG EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP TLKDPAKALETNTHVKCFSLAATRSNDPVATAPAEMLKVNKTLK SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE LEMAKMLEENTNILKPGYQFTQQGPRTRAANAITKNNDLVRKRR VEGDHQ
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL KMEKSKDTYLLVEGRGPGGSSLLIEALSNSSHKCQADIRHILNK NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG AEDVKETEDEERRNVPKPICDASSLHQVRKKLDSLGLCSVSCAL EPIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVVDNIE
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR KLPHSKAKTRSRLEVAEAEEETSIKAARSELLLAEEPGFLEGE DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG RHLAPGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL AVAQNRWLHIYDNQGIBLHCIRRCDRVTRLEPLPFHFLLATASE TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG TVSLWSPAMKEPLAKILCHRGGVRAVADSTGTYMATSGLDHQL KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA GQGKASPPSLEQPVLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR KLPHSKAKTRSRLEVAEAEEETSIKAARSELLLAEEPGFLEGE DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG RHLAPGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AVAQNRWLHIYDNQGIELNCIRRCDRVTRLEFLPFHFLLATASE TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG TVSLMSPAMKEPLAKILCHRGGVRAVADSTGTYMATSGLDHQL KIFDLRGTVQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR
6254	155	1139	HALGRRGGSQELSAAACGCFALRLRAPGSGRPALAPGAAAFAGL GGAPRFPPRGSAAGRTMLLKEYRICMPLTVDEYKIGQLYMISKH SHEQSDRGEGVEVVQNEPFEDPHIGNGQPTEKRVYLNSKLPSWA RAVVPKIFYVTEKAWNYYPYTITEYTCSPLPKFSIHIETKYEDN KGSNDTIFDNEAKDVERFVCFIDIACDEIPERYYKESEDPKHFK SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV EKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK VCNQHSSPVDDIESHAQTST
6255	1	1444	PTRPQQELLVSLAFVIFVASQKALSVESKAVIKQQLESVSNGWT VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPLNP LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTL GNDLQRCGRISNQMKQSMEEFRSLASRYGDLYQASFDADSATLR NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL SFQRYFFQKLQSTSIKLALSPSPRNPAEPIAVQNNQQLALKVEG VVQHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM EQRVEPHNDYFSTQFLLNPAILGTHNITVESSVKDANGIVWKTG PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA VDEQEAAAESLSNLHLKEEXIKPDTNGAVVKTNANAEKTDEEEK EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL RLKPQLLQGVYAMGFNRPSKIQENALPLMLAEPPQNLIAQSQSG TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK FIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQMLLF SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN
6257	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEPQRAQAAKAGAPG KA
6258	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEPQRAQAAKAGAPG KA
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH QRALTKDNPYEYNEYGEIPCDNSAPIIHQGAYTRKILREYKVSD KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHQRTHTGEKP YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL IVHQRTHTGEKPYKCNECGKTFCEKSALTKHQRTHTGEKPYECN ACGKTFSQRSVLTKHQRIHTRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPNI VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKQQPGPWPG MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS NVQRNRLVQHDLQVAKQLQSEDLKAQAQLQKRYKDLEQQDCEIA QEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA EIARKLQEEELLATQVDMRAAQVAQDSEIARLLMAEEKKAYKKA KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPA RPPPPIMTDQEDADYTHFTNQQSSTRHFSKSSSSHKQFHYKH
6262	2	1759	PECHSQGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL GSTRLVSQGLEALRSEHQAVLQSLSQTIECLQQGGHEEGLVHEK ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR LCQENQWLRDELAGTQQRLQRSEQAVAQLEEEKKHLEFLGQLRQ YDEDGHTSPEKEGDATKDSLDDLFPNESEEDPSNGLSRQQGATA AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN PNVARTKNNLASCYLKQGKYAEAETLYKEILTRAHVQEFGSVDD DHKPIWMHAEERSEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV NTTLRNLGALYRRQGKLEAAETLEECALRSRRQGTDPISQTKVA ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSQTLQR SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLYISEGRPT IEVRRCSMPSVICEHTKQFQTISSESNQQSLLTVPGDTSPSPKP EVPSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT APVNTVMDSPVHLEPSSQVGVIQNKSNEMPVDRLETLSTRDFIC PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAQ DPASFMPPQQPCSFPSQSLSDASSISKHMSLSYVANQEPGILQQ KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAPVPVYSDST IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ QSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKANTMA NQSKQILASCTLLSSKDSESSSPRGRIRLTSDDDPQIHIPRKRK VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER ANPYPEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLQHSIE REKLIVSNEQEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ QHEAAALNAVQRLEWQLKLQELDPATYKSISIYRIQEFYVPLVD VNDDFELTPI
6264	143	1960	KHRQENNALEMAPEIHMTGTWCLIENTNGELVANFEALKILGAI TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL SSTLVYNSWGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLSLVLTY INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLPQKKLAAQL DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLPQKKLAAQL DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRSPQDGNQQPAPPEKVGWVRKFCGKGIPREIWK NRYVVLKGDQLYISSKEVKDEKNIQEVFDLSDYEKCBELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEERPTSLC
6268	160	1368	HRELCQNLPAGLSSALIDNPLTLLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS
6269	2886	1449	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSPGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMASLGA HDPQTTQELLTTLRDASESPGENCQHLLARDVGLPLCQALVEAE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQ
6270	23	2086	SVTVTLSSEGDCRPPTVHLEEMEQEFQNGEPAEIKYIREAVKKA FLFVNKGLNTDELGQKEEAKNYYKQGIGHLLRGISISGKEGEHT GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDNLYPLVPDRSPVLK CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELPEDLLRQMS DLRLQANWNRAEENEFQIPGRTRPSSDQLKEASGTDVKQLDQG NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPEEKPKELPEW SEKVAHNILSGASMVSWGLVKGAEITGKAIQKGASKLRERIQPE EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGPATHHAVDSAV NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ EGAANVNVRGEKDEQTKEVKEAKKKDK
6271	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVEEEVNIPNRRVLVTGA TGLLGRAVHKEPQQNWHAVGCGFRRARPKFEQVNLLDSNAVHH IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKEA AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTPHWSGNEQM TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
6272	1136	528	GAVMEDAAAPGRTEGVLERQGAPPAAGQGGALVELTPTPGGLAL VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGQ QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKI SMMDTLLSQSVALPPCTEPNFQGLTH
6273	256	843	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCNGRPQDLKIA SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNBIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT
6274	56	1142	AAAAMAAAAGGGAGAARHLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQBYKKDPDRGYGAGVVTVPKKLLNPKCR DVPEPARAQPNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVIILALQGESSSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLERVFQKS
6275	20	565	SRRGRARCLARGSRRPVPRPAKTMAPMVKTHVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEVEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE KCHVM
6276	797	97	TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP VWVGAKISHGSPSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV LGSGYREQLLTDMLELCQGLWQPVSFQMQAMLLGHSTAGAIGRL LASSPRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYYRLPQ GYHKDLLAHVGRN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6277	4600	2744	MAFRTEMGLYYSYFKTIVEAPSFLNGVWMIMNDKLTEYPLVINT LKRFNLYPEVILASWYRIYTKIMDLIGIQTKICWTVTIGEGLSP TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGL VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQMLLVTHILRA TKLYRGSLIALCISNVFFMLPWQFAQPVLLTQIASLFAVYVVGY IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVPQNSVYKVLEVV KE
6278	3	823	YLFRLVLLSIVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKQ YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA PVPSACFRNICKQMTKMHEAIFDLLPEEQTQMLFLRINASYKLH LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN MAEIWEQXR
6279	117	1687	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA AESLNSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQKPRPEAE PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSERRASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYPAPI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFERI LFIWAIRHPASGYVQQINDLVTPFFVVFICEYIEAEEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEKKDFQELLLFL QNLPTAHWDDEDISLIIAEAYRLKFAFADAPNHYKK
6280	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRNLHQRERGLCHRGSFSLGEQSRVISHFLFNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSGR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ
6281	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSGR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALRRLRGASVTIR FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKQ VRPMLLVDDRALPDFKGIQTSDPNAVVMQLAPEHFHYQILNQAF RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGML GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILQHLL
6283	140	1043	LSLPGIHVMNPFWSMSTSSVRKRSEGEERTLTGDVRTSPPRTAP KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPPYLEYSLL AEFTLVVKQKLPGVYVQPSYRSALMWPGVIFIRHGLYQDGVFKF TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR RNHMHIWQVLMYARRVFYKIDTASPLNPEAAVLYEKDIQLFKSK VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
6284	1	2079	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL VSIDAAEIADGNPSLVLGLIWNIILFFQIKELTGNLSRNSPSSS LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST RENLEKAPSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQPL ERPPELEAEDIFDSDKEVPIESTPVRIKETPSEQESKVPVLTEN GERTYTVNHETSHPPPSKVFVCDKPESMKEPRLDGVRSHALSDS STEPMHQIIDQVLQGGPGKTSDISEPSPESSILSSRKENGRSNS LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE EGDYPEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGEEA EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLQGVG EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPLSKVSVIPHDLF YPPHYEVPLAAVLEAYVEDPEDLKNBEMDLEEPEGYMPDLDSRE EEADGSQSSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP LAPHEDHQQRETKENDPMDSHQSQESPNLENIANPLEENVTKES ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
6285	2157	1331	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHH IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVH ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVINCG VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA EWSMSFSPFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN NERTRLLSRDI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAWAQLQTRFVTDNKKVAVDDV PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGQFLRM PLDKHMEMENISSEVVEIEYVEKYTAPQPEQCMFHDDMISSIK GAEEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKD SLSCLLLSASMDQTILLWEWNVERNKVKALRCCRGHAGSVDSIA VDGSGTKFCSGSWDKMLKIWSTVPTDEEDEMEESTNRPRKKQKT EQLGLTRTPIVTLSGHMEAVGSVLWSDAESICSASWDHTIRVWD VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TTSHVGA
6287	278	1482	MQFFFNFQIGLRSTSGKEKYSGDAGPLGDALQLFLQCLALDEDP APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT QLLIELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA YPTVPCPLHVFEPRYRLMIRRSIQTGTKQPGMCVSDTQNSFADY GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE YLEDV
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNVCSEAAQKRSLDR
6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM EMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNVCSEAAQKRSLDR
6290	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRMISRYTRKA VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS DITRESSPTSADTGNSLSAFPSYTGAGISTEGSSDFSMGYGELD QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY LAFDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VPDSVNCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P
6291	1732	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PPAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQQSSAS3APQSVKRKAPDADDQDVKRAKATLVPQVQPST SANTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL
6292	1835	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNPSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVNSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL VGSRTLPVDPHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVVTEGGNFEEGMK LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY HASSHAIFPATPCQKNDIELTPPKGYEAQTFNWENYLEKTKSKA APSRLPNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRL LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQQLQPPVAAEP ATPLKAKEATKKKKKQPGKKRKRIPPTKTRPLRQQSKKPLLEDD PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE NIKQETDD
6294	354	1814	AQLTTRGRTVAGGVRWIPSPPPDLELYSCCLGTDRQFPELSHHC KNVIATASDYDMAEITNIRPSFDVSPVVAGLIGASVLVVCVSVT VFVWSCCHQQAEKKHKNPPVKFIHMLKGISIYPETLSNKKKIIK VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKHRR VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRPS RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGGLQV SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVMVYYGRK RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS EY
6295	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK TRRLSSSESPQRDPPPPPPPPLLRLPLPPPQQRPRLQEETEAA QVLADMRGVGLGPALPPPPPYVILEEGGIRAYPTLGAECPGWDG TIESGYGEAPPPTESLEALPTPEASGGSLEIDPQVVQSSSFGGE GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMRSSR RRRRRRRRKQRKVKRESRERNAERMESILQALEDIQLDLEAVNI KAGKAPLRLKRKPIQMRRPPLERRDLIIQHIPGFWVKAFLNHPR ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT NMVIVKEPQRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDASHS FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYLRRRGSRIKRKK QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK ISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDN NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNNENTY GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIDEARCCVWLLDGTTV EAVRPARERLARKELRQKRMQQPSRDSAVSSNKDSTCLLTERDT LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK KWALIHKRVRLSVFGARWGRIYFGK
6297	1	922	QRAAAASPSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGPLS VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAII VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVN NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTPPPEGV FVNTLGLLILVPGALIFWIVTRPQWKRPKEPNSTILHPNGGTEQ GARGSMPAYSGNNMDKSDSELNNEVAARRNLALDEAGQRSTN
6298	3	985	SVPLRRLSLSGTLQQAGTTTKMAVARLAAVAAWVPCRSWGWARV PFGPHRGLSVLLARIPQRAPRWLPACRQKTSLSFLNRPDLPNLA YKKLKGKSPGIIPIPGYLSYMNGTKALAIEEFCKSLGHACIRPD YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGGSLGG WLMLHAAIARPEKVVALIGVATAADTLVTRFNQLPVELKKEVEM KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVHCPIRL LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRNREKADI QLLVYTIDDLIDKLSTIVN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6299	512	814	RCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ MKEEEVQLRNNH
6300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWRQGARA AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGGPR LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE WFEVNRSCPEHPSD
6301	616	284	GKFVPVNWEPPQPLFPPKYLRCYRCLLETKELGCLLGSDICLTP AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	IPGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNEYGGGLLWQSWQEKHPGQALSSEPWNPPDTKEEWEQHYSQL YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS HRQVRVLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV PDEQDCVTQEVPDSRQAETEAEVKKKKNKKKNKKVNGLPPEIAA VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA TAETFDIRTMMSPDGPEIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
6304	1	1438	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL CGLIKRPGDLPEVLSPHVDRVLGLRRSLPAVARRFHSPLLPYRY TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
6305	99	420	NHIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES RDPAPGQEREEDQGAAETCVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMPEGR
6306	1	1874	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVQ SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCPEIVTANA TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER YITHESDDARNEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LAERISVL
6307	2136	589	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKFRHVPG QPVKNDQCYEDIRVSRVTWDSTPCAVNPKFLAVIVEASGGGAFL VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWIPTARNVLL SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS ACKDKSVRIIDPRRGTLVAERKAHEGARPMRAIFLADGKVFTT GFSSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG PEAALEAEEWVSGRDADPILISLRKAYVPSKQRDLKISRRNVLG DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	2	1118	GRPTRPEKMLLSLVLHTYSMRVLLPSVVLLGTAPTYVLAWGVWR LLSAFLPARPYQALDDRLYCVYQSMVLFFPENYTGVQILLYGDL PKNKENIIYLANHQSTVDWIVADILAIRQNAIGHVRYVLKEGLK WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLQSYVDAGTPMYL VIFPEGTRYNPEQTKVLSASQAPAAQRGLAVLKHVLTPRIKATH VAFDCMKNYLDAIYDVTVVYEGKDDGQQRREPSTMTEPLCKECP KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD PERRKRPPGKSVNSKLSIKKTLPSMLILSQLTAGMLMTDAGRKL YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA VMDVVNYFRTVGFEIQASAFQEQEIDGKSLLLMTRNDVLTGLQL KLGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	GPRCWKFLYILSSVNCETLRIGKAWPQSSGQERYWTFRTHSSASE AQRGSLASLNVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS VVDHFHSSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP CIPKIQSMIEDAWKEGFDPQGASQLIIRILQGTKAWIGACEVYIL LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN MVPPKVKCLTKIWIPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI KRYAR
6312	213	1400	GDELVKREAGMKALPGVGVPGTGSSARVLVPLLRAEGFTVEALW GKTEEEAKQLAEEMNIAPYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRABKVHGLLKTFVRQNAA IRGIRHVTSDDFCPFQMLMGGGVCSTVTLNFNMPGAPVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
6313	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVPMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEP TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNRAKKRKIARTSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAARED HED AEDLETKPTVDSEAEKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSPHGCWFYPVVVPMPLGVL FHRRRAHGCTLSCSSFVEQPTAMSAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHPKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCFSDPTSK QVEGIEIVELQLSHVKDLPHCEKCNRSFKLFYHFKEHMKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAARED HED AEDLETKPTVDSEAEKAENEDRTALPVLE
6315	1	1015	LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELFDHGCDSLSTVPMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTVVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
6316	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEELALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG
6317	102	839	PZAQTSAVLARERKGHLPTMRHEAPMQNASAQDARYGQKDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA EIEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319	88	717	AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLPLTDLEDLTLGBIEVMIAEPSCRGKGLGTEAVLAML SYGVTTLGLTKPEAKIGQGNEPSIRMPQKLHFEQVATSSVFQEV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYRETARSCNCYMEALALVGAWYTA RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS EDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALAEVTYHSSRCRGIQAF RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRMADPQISESNFSPK FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA IPGGMVDPGEKISATLKREFGEEALNSLQKTSAEKRBIEEKLHK LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM LEAGDDAGKVKWVDINDKLKLYASHSQPIKLVAEKRDAHWSEDS EADCHAL
6322	2047	1083	KQEILKNVESSRTVQPHPLEPLLSLGWSVDVGRHPGWTGHVSTS WSINCCDDGEGSQQBEVISSEDIGASIFNGQKKVLYYADALTEI AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIP IHPLNTGLFRIKIQGATGKPNMVIPLVDGMIVSRRALGFLVRQT VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEPYT SLPQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWYPRFPAGSPKGCPACVSKPPALQA PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARWGLEAPRGGRRRQPQQQ RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES PQAEPWTDQQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW SELGTTCLWTETGTDGLWTDPHRSDLQFQPEEASPWTQPGVHGP WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDQPLE EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS RVEGGSGGFSSASSFDESEDDVVAGGGASDPEDRSGSKPWKKL KTVLKYSPPVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNTNP KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPPRRKRRLKPQVKMSHYVNDMWPGSPQERDSPSTSRSGGS SRLSSRSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRSRRRHQ RKYRRYSRSYSRSRSRSRSRRYRERRYQFTRRYYRSPSRYRSRS RSRSRSRGRSYCGRAYAIARGQRYYGFGRTVYPEEHSRWRDRSR TRSRSRTPFRLSEKDRMELLEIAKTNAAKALQTTNIDLPASLRT VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHPSSGHIYVLMGLLPPPWTISFT VQTTLQPPGGLPAAPVSGRNAPEPVGRDLARRMVPRAGKRTQTL GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QAWGGVGQEASSGVP
6327	1	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKRKEEK GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEEEMHTDAKIRAENGTGSSPRGPGCSL RHFACEQNLLSRPDGSASPLQGDTSVLAGVYGPAEVKVSKEIFN KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT ELQQCLAAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNL RGDIERKSLAINEEFVSIFKEVKEELESISEDVQAMSNCCQDMT SRLQAAKEQTQDLIVKTTKLQSESQKLEIRAQVADAFLSKFQLT SDEMSLLRGTREGPITEDFFKALGRVKQIHNDVKVLLRTNQQTA GLEIMEQNALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKLMD KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS
6330	1151	333	FFYYTFYENKTFSRKMVAEKETLSLNKCPDRMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAPKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN
6331	3	495	QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1	878	VTESNKPDLVSPIPLLRERIYSNNQVARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPPCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GAKSMWTEHKSPDGRTYYYNTETKQSTWEKPDDLKTPAEQLLSK CPWKEYKSDSGKPYYYNSQTKESRWAKPKELEDLEGYQNTIVAG SLITKSNLHAMIKAEESSKQEECTTTSTAPVPTTEIPTTMSTMA AAEAAAAVVAAAAAAAAAAAAAAANANASTSASNTVSGTVPVVPEP EVTSIVATVVDNENTVTISTEEQAQLTGTPAIQDQSVEVSSNTG EETSKQETVADFTPKKEEEESQPAKKTYTWNTKEEAKQAFKELL KEKRVPSNASWEQAMKMIINDPRYSALAKLSEKKQAPNAYKVQT EKK
6334	17	644	GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNQNRSMEAHNILSKR GFSVRSPGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDK ELYTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYD QVVEDLNSREQETCQPVHVVNVDIQDNHEBATLGAFLICELCQC IQHTEDMENEIDELLQEFEEKSQRTFLHTVCFY
6335	82	529	AARARPGVLCCRLLGAALGDQSRVEMSYIPGQPVTAVVQRVEYH KLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEG GPAEIAGLQIGDKIMQVNGWDMTMVTHDQARKRLTKRSEEVVRL LVTRQSLQKAVQQSMLS
6336	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRNNGLGPESRYHLLRN LLTGLVRHERIEAPWARVDEMRQYAEKLIDYGKLGDTNERAMRM ADPWLTEKDLIPKLPQVLAPRYKDQTGGYTRMLQIPNRSLDRAK MAVIEYKGNCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS NHSSHTAQTPGI
6337	76	524	EGIQMLSVQPDTKPKGCAGCNRKYKDRVLLKALDKVWHEDCLKC ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKLI PAFEMVMRAKDNVYHLDCFACQLCNQRFCVGDKFFLKNNMILCQ TDYEEGLMKEGYAPQVR
6338	66	1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP GLRLALLLLLGLGTPKSGVQGQEGLDFPEYDGVDRVINVNAKNY KNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLED KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK DSEHYKAFEDAAEEFHPYIPFFATFDSKGAKKLTLKLNEIDFYE AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE DDMDGIHIVAFAEEADPDGFEFLETLKAVAQDNTENPDLSIINI DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDDD
6339	246	1813	NRCDRGGGGQAERQAGQGCRTQGAGPGPGFGHSFFSQGAMKAPH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDVNDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELEGQDENQEGDFEDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPIKLPDTKR TLLLTFNVPGSGNTYPKDWBALLPIMNMVIYSIDKAKKPRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM
6340	2	583	EACAHTLSCPAFARLGRARRRPWWSHRTSSTFRAERSFHSSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR MPHTEHVQQTFRTEIKI
6341	2	645	KMAVLSAPGLRGPRILGLRSEVGPAVQARGVHQSVATDGPSSTG PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PALRKVVDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLNTGRPQSDMNNI KPLEGVKILDLTRVLAGPFATMNLGDLGAEVIKVERPGAGDDTR TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC DVFVENYVPGKLSAMGLGYEDIDSIAPHIIYCSITGYGQTGPIS QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG TAHGSIVPYQAFKTKDGYIVVGAGNNQQPATVCKILDLPELIDN SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKPK MSEARPFPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	2	936	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESQPTLSKCIDAV MVLGNSHLFMNRSNKLAVIASHIQSSRFLYPGKNGRLGDFFGDP GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV PQMPSLLQYLLNVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL IEIGYVCSVCLSIPCNFSPICTTCETAFKISLPPVLKAKKKKLK VSA
6344	2508	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ PQVQPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ LQLQKQVQTQTPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP VGTQVSMEEIQNESACGLDVGECENNRAREMPGVWGAGGSLKVTI LQSSDSRAPSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCFEGDEEEEEDDEDEEEIEVEEELCKQVRSRDIS REEWKGSETYSPNTAYGVDPLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAARNPSPTTRPVSRRCAINARNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
6345	2	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTSRDQNEKLVQENREL QLQYLEQKQQLDELKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSPLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEPDETIHLERG ENLFEIHINKVTPSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNPGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVIYVDK ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME LAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCMVGRLNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSPLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6347	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCMVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHILWLEVLCSSLPTVEKWYQPWSPLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6348	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLTKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLRSGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCPLTQLACPLANQQNKYKYYEPCKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAPYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
6350	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACPLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6351	1291	319	KEARRRTERSQLGRMLVVEVANGRSLVWGAEAVQALRERLGVGG RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP DSRHHSLALTSFKRQQEESFQEQSALAAEARETRRQELLEKITE GQAAKKQKLEQASGASSSQEAGSSQAAKEDETSDGQASGEQEEA GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKPGGDPLVYPGD PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCBPQ PDGKVVYTSLQWASLQ
6352	235	923	WSEWLSFCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP DDCVYIVVD
6353	65	672	RFAGAGAIPEARARPPDVQAAEEEKEMDLPDSASRVPCGRILSM VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER PLHETRTLVEMKRDLDSIPRRIRTLKGKLARQHPEAFSHIPEAS FLEEEDEDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSLSPGFE DLSHVQPGSPAINGRSQTDDEEMTGE
6354	965	510	PSLRPMEPTRDCPLFGGAFSAYLPMGAIDVSDLRPVPDNQEVPC HPVTDQSLIVELLELQAHVRGEAAARYHPEDVGGVQGARAVHVE SVQPLSLENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLHQA LLRLPQYQTDLLLTFNQPP
6355	158	1662	RGSSAAPRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGPSLD WDGKVSEIKKKIKSILPGRSCDLLQDTSHLPPEHSDVVIVGGGV LGLSVAYNLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ QFSLPENIQLSLPSASFLRNINEYLAVVDAPPLDLRFNPSGYLL LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV ALASYGMEDEGWPDPWCLLQQLRRKVQSLGVLFCQGEVTRFVSS SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRVYVYVWHCPQGPGL ETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLEVDHD FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTPDQNGVVGPH PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPP LFTRFYLGEKIQENNII
6356	354	633	TGLTSSCLPLQVMMTKRTKDMGKPSSVTVSTIDEEEEEYEAREV ADSYAQNAKVIEKQLERRGMSKRRLQELAALEAKKAKMXGTLID NQFK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6357	2	915	GLLRNMALLVRVLRNQTSISQWVPVCSRLIPVSPTQGQGDRALS RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP QPVEEKVGAFTKIIEAMGFTGPLKYSKWKIKIAALRMYTSCVEK TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEGRSGKYM CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFYAAILGY DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATHTEQAISFAKDFLAGGIAA AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTE REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM MQSGRKGADIMYTGTVDCWRKIFRDEGGKAPFKGAWSNVLRGMG GAPVLVLYDELKKVI
6359	98	1096	VCRQEEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE GKSFQLRHRBEEGTLIIEGLLNIAWGLRRPIRLQMQDDREQVHL PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKAESSTDSS GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHRFS INGHFYNHKTSVPTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEEREIIKLT MKFQALRLTMLQRLEQLVEAK
6360	1	345	GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGNVFLKHGSELRIIPRDRVGSC
6361	615	158	RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC APGRWRRQITSQEFCHPIQGRCTFTPDDGETLHIQAGDALMLPA NSTGIWDIQETVRKTYVLIL
6362	350	1576	TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMQNMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE
6363	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6364	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1989	KHKSRASCAARAQAFGPSRERERVHSRFRSGLRRLGESNSGCCTM ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVA NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQIAK LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIRI ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV VNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK LDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLAICQWGFDDE ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCP TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVKEM NPALGIDCLKKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK IDDIRKPGESEE
6366	257	1898	GNKEGAH55TPWVLLSIFLGAVAMLCKEQGITVLGLNAVPDILV IGKFNVLEIVQKVLHKDKSLENLGNLRNGGLLFRMTLLTSGGAG MLYVRNRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALNFCLIGLIC QALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI RYYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQ PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKVPDCYYNL GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALPLKA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV
6367	287	1934	SIGFPVMLVLSILLYTCENFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVQT GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKP CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPII ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR
6368	1	327	RPVPAKLNPRSWPRTAGALDLRPPPLTMAVPIIDEVHIEDFQYDE DSETYFYPCPCGDNPSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHGSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SSLHIHERTHTGDKPYECKVCGKAFTCSSSIRYHERTHTGEKPY ECKHCGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE HERTHTINR
6370	1711	329	FVLSEQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG ALVGGLRPVTMTTPANAQNASKTWELSLYELHRTPQEAIMDGTE IAVSPRSLHSELMCPICLDMLKNTMTTKECLHRFCSDCIVTALR SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSREEYEAHQD RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY LALRIALERRQQQEAGEPGGPGGGASDTGGPDGCGGBGGGAGGG DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE KFWKVSRPLELCYAPTKDPK
6371	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC LHNNNFENALCRKESKEYLECRMERXLMLQEPLEKLGFGDLTSG KSEAKK
6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKNPSLQPVVMCVMKH LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGQE QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLNSFLVD DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY YVLHITKQRNKNALLRLLPGLVETFGDLAPGDIFLHLLTGNLAL LADEPALEDPCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAETFTDIPLCWPPFYYELKIAPVA WLLSPYTKGSSLLYRKPVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
6374	535	2105	HKLFCSYISTSEPPSSTRHHSCPTHTFCNYTSSTIPLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPCSQVLVRVDWERRFDHMQQH SQQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEITLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRPQGKATKMSRRMEAQALLQDYISTQSAKE
6375	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGIPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDFHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLLSLAVLIVVFSLFMLTFSTSP GQESPVESFIAPLLIELACGLYFPSMSFLRRKVIPETEQAGVLN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV VGLFTVVRHDAELRVPSPTEEPYAPEL
6376	380	1437	ISSTDIDHYRPSFLVNSKNPSKESWSQRKTNRAAVHKSKQEGRQ QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKS NEQIPKYEKIHNFKVHTPRGPHWCBYCANFMWGLIAQGVKCADC GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM VVDMCIREIESRGLNSEGLYRVSGPSDLIEDVKMAPDRDGEKAD ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKPIESSAKIMD PDEQLETLHEALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA ENLGIVFGPTLKRSPELDAMAALNDIRYQRLVVELLIKNEDILP
6377	2311	1845	SRIRRRSSRRPRRPPGPSRRRRRRRPDPRTWPSEKTFKQRRTPE QRV3DVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHV NMSELIKIIRRRLQLNANQAPFLLVNGHSMVSVSTPISEVYESE KDEDGPLYMVYASQETPGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6379	35	378	ERAGSPSPSRAALRRCAPQHSQAPRWPDRAACRRSPQGSQGRAY LFNSVVNVGCGPAEBRVLLTGLHAVADIYCENCKTTLGWKYEHA FESSQKYKEGKYIIELAHMIKDNGWD
6380	1414	462	PAVQGQRGAGPPTGRGSGNMARPALTVVRHGETRPNKEKIYQGQ GVDEPLSETGFKQAAAAGIFLNNVKPTHAFSSDLMRTKQTMHGI LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREB CPVPTPPGGETLDQVKMRGIDFPEPLCQLILKBADQKEQFSGGS PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLPIINFBEG REVKPTVQCICMNLQDHLNGLTBNSLGLNLPSKSNHFSPLKGVP LALFTSLLC
6381	1668	218	AVVRAQGSRGFSGAGWRPRQAAAANNFSEVPKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLPILC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAPSPDSYFLATRNDNIPNAVWVNDIQKLRLPAVLEQL SPVRAPQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
6382	2	1062	PEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEPEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCKQQQIQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDARDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E
6383	3159	1061	SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHCAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVARK PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAAAASSSASCSRRLGRALNFLPYLALVAAAAPS GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKDLSDGIHVVKDARERDPTSLENTVBERLTELTKSYNDNIAYF TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSL GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQA QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQFLPFPSSSINEEDADEANRAIGEKR AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP SNIGAPLISSMGTTNVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ QQQMQQMQQQQLQQHQMHQQIQQQMQQQHFQHHMQQHLQQQQQH LQQQINQQQLQQQLQQRLQLQQLQHMQHQSQPSPRQHSPVASQI TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD LHRQFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAQAP IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFNCAFSRTLPWSSVL RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER LRSLSPKIMQEAPLVQEVVELPVTERQIEREHLIQLRRWQETRG ELQCRSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQEEEDTYL
6386	819	195	TVCGSFYLGIMQNASRLKRELHMLATEPPPGITCWQDKDQMDDL RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRPLTPIYHPN IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEESMLDNL PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGNDRYLTNQK NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6388	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6389	1074	497	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKPKKLLVPGKIQHI LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ LIGDDVKVERIEYKKP
6390	158	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA MSLLGSRNQLARAVLNPNPMDPCTKDLLTTTSERIIAYLRDFNE DQKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKRIYLEF KEKCKDKKNPLGNCGDINLVRLGPEKSINSEVLKFSLDSQVNHR MKKELPSHVQAMHKRKEFLDYQLDELSRQRALCRGGRSIQRQEL DENISKVSKERQELASKIKEVQQRPQKTQSIIILESHIICCTLS TSGGLLLESAFRGQQGGVPPSCVIVDEAGQSCEIETLTPLIHRCN KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVEHN MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC SSDWPFQPYLVFDVGDGSERRDNDSYINVQEIKLVMEIIKLIKD KRKDVSFRNIGIITHYKAQKTMIQKDLDKEFDRKGPAEVDTVDA FQGRQKDCVIVTCVRANSIQGSIGFLASIQRLNVTITRAKYSLF ILGHLRTLMENQHWNQLIQDAQKRGAIIKTCDKNYRHDAVKILK LKPVLQRSLTHPPTIAPEGSRPQQGLPSSKLDSGFAKTSVAASL YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGQ IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAPSE GEQEKCGSETHHTRRNSRWDKRTLEQEDSSSKKRKLL
6392	972	186	GRTGVDLASSMAHRLQYRLLTWDVKDTLLRLRHPLGEAYATKAR AHGLEVEPSALEQGFRQAYRAQSHSFPNYGLSHGLTSRQNWLDV VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPCTWQVLDQAEDTLR ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSPL VVGPQALDPVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
6393	2017	730	TGGSKMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGTV LLIEEDKYNIYSPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ ELPAPLLDDKCKKEPDEDVYNHKTPESNIKNKIAWRYQLLPKMS IGPVSSSRFGHYYDASKRMPQELIEASNWHGPFLPEKISSTLKV EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN LGSPLWGDDICCAENGGNSHSLTKPLYVLRGLLRTSLSACIITM PTHLIQNKAIIARVTTLSDVVVGLESPIGSERETNPLYKDYHGL IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGARRRPAAMATVMAATAAEKAVLEEEPRWLLHDEVHA VLKQLQDILKEASLRFTLPGSGTEGPAKQENFILGSCGTDQVKG VLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQQIQDAR NHVSQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLT TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC VIPWLNDALVYFTVSLQLCQQLKDKISVFSSYWSYRPF
6395	13	658	PSGRPTRPLCCAARRGAARHGGSVSGVPAGRTPTETSNPGSSVM ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ DLLEEASSRDMQMGPGLFLRMQLVPSIEERETPLTREDRPALQE PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE
6396	1	1221	ANILSSPSKRGQKGTLIGYSPEGTPLYNFWGDAFQHSSQSIPRF IKESLKQILEESDSRQIFYFLCLNLLPTFVELPYGVLTNSLGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGP INGLPLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQQSCHSSDHSHSHHMHGHSDHGHGHSH GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM
6397	391	122	GAGGVGRPEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTYGDLK KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYSIHDGMNLELYY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			Q
6398	353	1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK DIEAQKNYFRMWQKAHLANLNQGKVLPQNMTTTHAVAILFYTLN SNVHSDFTRAMASVARTPQQYERSFHPKYLHYYLTSAIQLLRKD SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQQFLSTSLLKEEA QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS VIIFSKSRV
6399	75	1245	PNLETVFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQKKMAECEAEN EDLLKKLELYKEACEGQHKLECDLQQREEEIAELQKALSDMQVC LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT YPCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR SENQNKEKSWMLEKDNLMSKIKQYRVQCKKKEDKIGKVLPVMHE SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTNKCDEVVYEVQSAILRHNCGYAMKTGKFPHNLMERKDPETNL DNISVTFLSLTDLQKNETLDHLISLSGAVQLRHLSNNLETLLKR DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHEAFETS SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGQCVYGIQT HTCAAVKFDEQKLVTGSFDNTVACWEWSSGARTQHPRGHTGAVF SVDYNDELDILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLRTL SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK TPEIANLALLGPGDIFALLFDNRYLYIMDLRTESLISRWPLPEY RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW KEHG
6401	109	766	PGAAWSRPDLRGCCTGPQPALRMLVLFSPCPQPLAFSSVETMEG PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSYLQRHSITHS EVKPFECDICGKAFKRASHLARRHSIHLAGGGRPHGCPLCPRRF RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRNKHP
6402	1196	279	TTSQCGGIRQSSAIPVASMEPAAYCLRNALLLPEEQQDPKQEN GAKNSNQLGGNTESSESSETCSSKSHDGDKPIPAPPSSPLRKQE LENLKCSILACSAYVALALGDNLMALNAHADKLLQQPKLSGSLKF LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS DKGENEAMESSGKRAPQCYPSSVNSARTVNLFNLGSAYCLRSEY DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIQMPAFTTVQRK
6403	2	1690	RGIHTSVLQGNLQNQNYSHNVVIMNLNNLNLTQVQQRNLITNLQ RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNLK DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMRSRLDTEVANLSVIMSEMKLVDSKHQQLIKNFTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP GKEGLPGPQGPPGPQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNPTDKCYY PSVEKEIPEDAKLFCEDKSSHLVPINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL
6404	1012	222	AAALAMAAPAPGLISVPSSSQELQAALAQLVAQRAACCLAGARA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV PFDHAESTYGLYRTHLLSRLPIPESQVITNPELPVEEAAEDYA KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQERKKI VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGEGKAAVLKRI LEDQEENPLPAALVQPHTGKLCWFLDEAAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYMSMELLQE AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAQVLAGGRGKGT FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQ VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE TPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK LYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQK KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKPQLP I
6406	1036	167	HPKQMRGEDTPEAPPYSSGRVDSIKTEVSGCPEDLTVGRAPTAD DDDDDHDDHEDNDKMNDSEGMDPERLKAFNMPVRLFVDENLDRN VPISKQPKEKIQAIIESCSRQPPEPQERARKRIRTYLKSCRRMK KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYQ SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSMV CRAALGSGMGRGKQRPVMERGCLTA
6407	492	150	VGLCLAVSQTVLAQLDALLVPPGQVAQLSCTLSPQHVTIRDVGV SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	RGCITSSQAWRLPGGVTRGFNMRIEKCYFCSGPIYPGHGMMPVR NDCKVFRPCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN SFEFEKRRNEPIKYQRELWNKTIDAMKRVESIKQKRQAKPIMNR LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE DVDMEDAP
6409	150	446	NTALANLLRCPTCDRLCGGCTAPAPPAHQGIVLQPVNPSCDPGP GPACLPTKTPRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS HGRAYLPNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAPPAGSACLPADSCPCLLPQAC AISGLPNCITIHPLNIAAGVWMINNAPILLLCEAPFCCQPIEPA NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAPA TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
6411	302	772	RLSIMASSLNEDPEGSRITYVKSDLPACPKTDSLAHCISEDCRM GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK KRASHKPTYENLQKSLEAMKSHCLKQNGVTDLSMPRIGCGLDRLQ WENVSAMIEEVFEATDIKITVYTL
6412	61	1709	RPVTSPSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQ GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYRSKRKQN PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG RILSGNPFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP VALSNQGLPIGLQFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE LMDDCSAVLENEKLASVSLKQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFAIMGETVMSVKIIR NRLTGIPAGYCPVEFADLATAEKCLHKINGKPLPGATPAKRPKL NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEPFVKVYPSCRG GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF MEQSEELYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGFDRYKMVVQV VIGEQRGEGVFMASRCFWDADTDNYTHDVPMNDSLFCVVAAPGC FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAPRAP FIBAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLQE NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD TVQSELEEKIRRLEEDRHSIDITSELWNDELQSRKKRKDPFWPD KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV ITTINHDEVWFKRPDGSKSKLYISQLQRGKYSIKHS
6416	410	1519	EIAPADLEIPACAPVLLSRATSSTHSVTGGKMAPSLTQEILSHL GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLESRIVM ALLQPTAQFDAQELRTALKASDSAVDVAIRILATRTPPQLQECL AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV KGDCQSALLALCRAELM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAPVIACVLS LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT KCVSPTLTIEQFM3KFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA AHTNRKEYTLMKAYRVA
6418	2	662	TRTEPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH TPAPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQEAELVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRQRQ TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELESDRAEGLTN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV FWNLVWYFRRLDLPSNLPGLILSSEHCNKYSKIPRHCMSEDSKY VLIQMLNDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PAPMYGGFPVKLRTYLGDFIPYDPQITAEELAEKTKNAVQALID KHQRIPGNIMSALLERFH
6421	1844	362	WALSLRRQPERMSNKLLSPHPHSVVLRSEPKMASSPAVLRASRL YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCCW DEPVRIAVRGLAPEQPVTLRASLRDEKGALFQAHARYRADTLGE LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA VELEVLDGHDPDPGRLLCQTRHERYFLPPGVRREPVRVGRVRGT LFLPPEPGPPFPGIVDMFGTGGGLLEYRASLLAGKGFAVMALAYY NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPGVGLLGISKGG ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGETLPPVGVNR NRIKVTKDGYADIVDVLNSPLEGPDQKSFIPVERAESTFLFLVG QDDHNWKSSPYANEACKRLQAHGRRKPQIICYPETGHYIEPPYF PLCRASLHALVGSPIINGGEPRAHAMAQVDAWKQLQTFFHKHLG GREGTIPSKV
6422	181	2133	EGENLSWFQEPWGDIAKEPYWKTPCPQPFLRYNFDVTKGKIFIE WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTQITY HQLLVQVCQPSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL KELADEALQKCQEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI KRSCPDVQISWNQQIDLWWHELMQEAGDECEPEWCDAEDPLFIL YTSGSTGKPKGVVHTVGGYMLYVATTFKYVFDFHAEDVFWCTAD IGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTVGEPINPEA WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT PPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE RFETTYFKKPPGYYVTGDGCQRDQDGYYWITGRIDDMINVSGHL LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV LRKIAQNDHDLGDMSTVADPSVISHLPSHRCLTIQ
6423	614	1237	ANLXEIPRDLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLS KNGIEFIDEHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP FLNAANDADLCNLPKKTTDYAMLVTMPGWFTMVISYVVVYVRQN QEDARRHLEYLKSLPSRQKKADEPDDISTVV
6424	1	1188	KKVSWPVAAMVHCSCVLPRKYGNFIDKLRLFTRGGSGGHGYPRL GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKGSKGKDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGGL GGKLLTNFPLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGPQLSSHTQYRTAPETII LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP KDPLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII
6425	1850	1144	LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWRPLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA WREGVHGSAKFYISDLWKVTPSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPPFPHWTPDHVTGEGIDTVWAYDASTPRGRE KRPCTSMHFQLPIQA
6426	30	565	SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRPSFSPEPTLEDIRR LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST
6427	145	959	AASWGPPHVPRAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK NIREYVRMMMYWIVFALFMAAEIVTDIPISWPPFYYEIKMAPVL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVQAKERSYETV LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDA PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT VPSDVDS
6428	1982	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDLLKGTEAST KNIFGRYSSQRMKDWQEIIALYEKDNTYLVELSSLLVRNVNYEI FSLKKQIAKCQQLQQRYSRKEEECQAGAAEMREQFYHSCKQYGI TGENVRGELLALVKDLPSQLAEIGAAAQQSLGRAIDVYQASVGP VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY TETRNQFLDELMELEIFLAQRAVELSEEADVLSVSQPQLAPAIL QGQTKEKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVPANGTL VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG IPTPRVLWAPPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQQRFSWTLPNGMHLEGPQTLGRVSL LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTPVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRXNRKLGPGAGAGPGVLRRPRPTPGDGERRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSEQEMRVMDEDIMVESGDDSWDLITCYCRKPPAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP
6431	3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLRFEEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYPTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN MALDDVVILNVDTNTLETPPDDLQSLPNDVISSLKNRLKKVSTT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TGDGVARAFLKAQAAFFGSYRNALKIEPEEPITFCEEAFVSHYR SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVPEEEINM GEYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHPGQVR PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL LPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV PLAMEEWHHERKHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6434	40	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALPQFAEISSN TSQLGGAEPVKRCGKSALPQLAEMCLASEGMKNEESKLIKAKES DGGRIKELEKGKEEKEIKMEKTDETRLQKEAEPEKSAKENLRDS KELRNFEALQIDDIMAIKNEDPKEIRKEELEEDHKCSHFPDPGY SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK KSKMDRHGNDKSTPXKTCKKRQSSESDIESVIYTIEAVAKGDNG IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSREKKMSKEKS SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS LRANVDRGKRSSGKGNSSDHEGCWNEESNTFSQSGTSGSKKFKK TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK KKTGNVSSEPTKTSKGSGDKWSNKQLPLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA
6435	2227	657	ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPRENALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYSEATPWRWQGHSDVDPA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLPENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
6436	1295	341	GACRPPVRQDPDSGPDVEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK
6437	1828	360	PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVPLQIKNMVK LIHTLADHGDDVNCCAPSPSLLATCSLDKTIRLYSLRDFTELPH SPLKPHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCQ SVKDGSLAACAFSPNGSPPVTGSSCGDLTVWDDKMRCLHSEKAH DLGITCCDFSSQPVSDGEQGLQFYRLASCQQDCQVKIWIVSPTH ILGFELKYKSTLSGHCAPVLACAPSHDGQMLVSGSVDKSVIVYD

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TNTENILHTLTQHTRYVTTCAFAPNTLLLATGSMDKTVNIWQFD LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEELRTKVKS LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN RTSPP
6438	109	901	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6439	23	412	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL KQAKEEAQMEVEQYRRERHEHFQSKQQAAMGSQGNLSAEVEQAT RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3	517	RARWNSDMGDLPGLVRLSIALRIQPNDGPVPYKVDGQRFGQNRT IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
6441	234	1373	KSGGLRRRQRFGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY RNVCKENSTVGMKIQEELQRSGGLDHLVLSPGEWPVSDNTIMHI ATAEALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC AQLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKPERLET LIEVSVECIRMTHNHPTGFLGSLCTALFVSPAAQGKPLVQWGRD MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK DSENKAIFPDNYDAEERKTYRKWSSEGRGGRRGHDAPMIAYDA LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK GLYQDLEDKEKLEDLGRALYRLSTEEK
6442	34	796	AEDFAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGSARPGPC EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
6443	2	555	MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRKKRQ KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE VPSFTMGR
6444	390	899	GSTPRGKMRAPIPEPKPGDLYEIFRPFYRHWAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
6445	2	753	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVFNFLKDMARACQNYLKKT
6446	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDCADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LYQAMDIIRLNKLEDTITLIKGKIEEVHLPVEKVDVIISEWMGY FLLFESMLDSVLYAKNKYLAKGGSVVPDICTISLVAVSDVNKHA DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN RVVFSTGPQSTKTHWKQTVFLLEKPFSVEAGEALKGKVTVHKNK KDPRSLTVTLTLNNSTQTYGLQ
6447	1554	1068	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCQRVMNP SRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIA LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL PGFYHLRIAYYASKGYRGYSYDDIPDPDD
6448	74	559	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEBTEEFGLQK FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER QFIVRKVHYDPEKDVHIYEAQKRNQKEDL
6449	597	1876	EYGVCENLRKLEITGVSCRDVYAKLLHRYRHILGLWQPDIGPVG GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA ATVECMYGHKGPHHGHIQIVKKDEFSTKCNQTDHHRMSGGRQEE FRTNLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG DPNIPAGQQTVEIDLRHRIQLPDLENQRNFNELSRIVLEVRERV RQEQQEGGHEAGEGRGRQGPRESQPSPAQPRAEAPSKGPDGTPG EDGGEPGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRTCRM CFYGTGLIAGHGFTSPERTPGVPILFDEDRFGPVWLELKSPSLY SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848	269	FVPAPRTVSGKRSLPGEWEERGEGEQRTGREFSGNGGRAVEAAR MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPMQSFQGNQFQGEWP VLGLAGNSPRPEHRALLNAFTATFELSDDGRFEVNNAMTRGQHC DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS RDAGPVHLPGQSSGPLG
6451	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMQE ILPGLFLGPYSSAMKSKLPVLQKHGITHIICIRQNIEANFIKPN FQQLFRYLVLDIADNPVENIIRFPPMTKSFIDGSLQMGGKVLVH GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE EEDDFGTMQVATAQNG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCQ LTDRNYLGLKELHKEPGPSHPSVLAPPCNQPGESEPRPSKEVES FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK YLVNPEGQVVKPWRPEEPIEVIRPDIAALVRQVIIKKKEDL
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRHMGVWTDVHRRFLQL LMTHGVLEENDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFARNELDLP RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKBAEQVLQKP VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK VPDPEKERESGVLKSNKKSLRSRQH
6456	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKDA TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA DIFQNFSV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY SFLTLSSQLKPKPVGEENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY SFLTLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY SFLTLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMVF LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV APLEVQFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC STLFKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI QNGPIKSNGQEGPLLGTDSTGNVRTGLNKHETTV
6462	3	773	SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH PDSQSMEESKLKNDDRXTPVNWKDSRGTRVAVSSPMSQHQSYIQ YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGPHYPVYG KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA PVEKATAERERRAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
6463	2	350	VILCILGGNIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD LHQAEEDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYELL NKRRSVRFISNEQVPMEVIDNVIRTAGL
6464	12	1154	GILRQKERREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LVEPSKLGRTLIHEHLAMTFDCCYCPPPPCQEAYSKEPIVMKNL YWIQKNAYSHKENLQLNQETBAIKEELLYFKANGGQALVENTTT GISRDTQTLKRLAEETGVHIISGAGFYVDATHSSETRAMSVEQL TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH AQAQLGCPVIIHPGRSSRAPFQIIRILQEAGADISKTVMSHLDR TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFPKTLRNHWKKTTAGLCLLTWGGHWLYGKKCDNLLRRAAC QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTLFEKNAAPI LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGDGTLQEV VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVQHI TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN BPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ LSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFITIGSR KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEEYEAMPV EVKLLPRKLQFFCDPRKREQMLTSPTQ
6466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC PPCNHEKSCDVKMDRARNTGVISCTVCLEEPQTPITYLSEPVDV YSDWIDACEAANQ
6467	301	2571	GELRVLALAHGELACHAVLTASLLSLRSRLMD3DMDYERPNVET IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYQRSDV VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV VAQFGIKDVFDNAIRAALISRRHLQPWKSHLRNVQRPLLQAPFL PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI FAHKIYLSTSSSKFYDLFLMDLSSBGELGGPSEPGGTHPEDHQGH SDQHHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL LEVFDLRMMVANILNNEAPMNQEITKAPHVRRTNRVKECLAKGT FSDVTFILDDGTISAHKPLLISSCDWMAAMPGGPFVESSTREVV FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRNPPVWYLKE EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS SPSSSSAVV
6468	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLLPMLGLLQLLAEPG LGRVHHLALKDDVRHKVHLNTPGFFKDGYMVVNVSGLSLNEPED KDVTIGFSLDRTKNDGPSSYLDEDVNYCILKKQSVSVTLLILDI SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD GKGKFSRAHFVLL&LL
6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLLPMLGLLQLLAEPG LGRVHHLALKDDVRHKVHLNTPGFFKDGYMVVNVSSLSLNEPED KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL PFTKSLSLVFHAIDYHYISSQGFPIGGWAVVYYITHLLKGALLF ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD GKGKPSRAHPVLLSLL
6470	2726	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT QHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG SLQXTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEAIKFY RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYRAWHQ VEYYRYIRFPPDGHVMMLTTPEEPQSIVPRLRTR
6471	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALRRRRR GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLSEAPN EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILENTSK VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRRAQAR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQQRRREKA VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR RQARRRAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL
6472	3	897	SCGSDRAQWAMEPPFDVDALFPERITVLDQHLRPPARRPGTTTP ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKP LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
6473	22	912	SSAVEPVWEGEKMAAEPNKTEIQTLPKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTSLDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDPFTEHTQPPAN DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSPSEIERQAQVAE KLREQQAADAKKQAEESMVASMRLAYQELQIDR
6474	3	462	LQRQRQHPAAAPAVPVRCPTFCPTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN
6475	3	462	LQRCRQHPAAAPAVPVRCPTFCPTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN
6476	106	1090	ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL QGLRKDFLELRSAGVEQLMPIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF PASRWEAYDPEKKWDKYTIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6477	227	915	LQGHLMGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVL SEPVLFLKPSTAYAPEGSPILMPAYTRNLMHELELGVVMGKRCR AVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWTLAKSFTA SCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPV IISYVSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM TFKVEKPEY
6478	2	1495	FVSSRILPESLASSEASTLEAMGRKEEDDCSSWKKQTTNYRKTP IFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLEN EIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILE RGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPE ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA VDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFW EDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDI YPSVSLQIQKNPAKSKWRQAFNAAAVVHHMRKLHMNLHSPQVRP EVSNRPPETQASETSRPSSPEITITEAPVLDHSVALPALTQLPC QHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC SSCLNIGSKGKSSYCSEPTLLKKANKKQNFKSEVMVPVKASGSS HCRAGQTGVCLIH
6479	3	949	SCRGPGWHPAGGQAGAMELLSALSLGELALSFSRVPLPPVFDLS YFIVSILYLKYEPGAVELSRRHPIASWLCAMLHCFGSYILADLL LGEPLIDYPSNNSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL IFVAMKEVVRVRKIAVGIHHAHHHYHHGWFVMIATGWVKGSGVA LMSNFEQLLRGVWKPETNEILHMSFPTKASLYGAILPTLQQTRW LPVSKASLIFIFTLFMVSCKVFLTATHSHSSPFDALEGYICPVL FGSACGGDHHHDWHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK KKAKKAD
6480	192	514	DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY QIFPDPSDFDRCCKLKDRLPSIVVEPTEGEVESGSLRWPPEEFL VQEDEQDNCEETAKENKEQ
6481	110	1131	KSRMDLDVVNMPVIAGGTLAIPILAFVASPLLWPSALIRIYYWY WRRTLGMQVRYVHHEDYQPCYSFRGRPGHKPSILMLHGFSAHKD MWLSVVKFLPKNLHLVCVDNPGHEGTTRSSLDDLSIDGQVKRIH QPVECLKLNKKPFHLVGTSNGGQVAGVYAAYYPSDVSSLWLVCP AGLQYSTDNQFVQRLKELQQSAAVEKIPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVRIPHNNFYRRLPLSIVSEKSRYSLHQ NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD
6482	2517	568	EPVSKVSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFQA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVRLAVIEPHLGV NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI LNSERSEIETAQAYLESSEALYNQYMKEVGSPPLDPTERFLPEE EKLTEQERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHYCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGQTGKISATEDTPEAEGEVPELYHQRKGEIARCWIKYCLTLMQ NAQLSMQDNIGELDLDDKQSELRALRKKELDEEESIRKKAVQFGT GELCDAISAVEEKVSYLRPLDPEEARELPLLGQHYVPEAKEFPQ IDGVVTDHIEVVQDHSALPKGLAFFETDMSRRCKMHKRRIAMLE PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD SHIVKKINNLNKSALKYYQLFLDSLRDPNKVFPEHIGEDVLRPA MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP EAAQEIEVELELSKEMVSLLPTKMERFRTKMALT
6483	3	623	NSHLLCGLRARAPLSANGREARANEQRLAEFRAARKRAGLAAQP PAASQGAQTPGEKAEAAATLKAAPGWLKRPLVWKPRPASARAQP GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW LVLLGLFVELEFGLAYFVLSLFYWMYVGTRGPEEKKEGEKSAYS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VPNPGCBAIQGTLTAEQLERBLQLRPLAGR
6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF MILWLKGVKFNVTTVDMTRKPEELKDLAPGTNPPFLVYNKELKT DFIKIEEPLEQTLAPPRYDPHLSPKYKESFDVGCNLFAKPSAYIK NTQKEANKNFEKSLLKEPKRLDDYLNTPLLDEIDPDSAEEPPVS RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW RYLHNAYAREEPTHTCPEDKEIENTYANVAKQKS
6485	6	1091	FVDLVRAVEFLPCPDSQKLEKECQSSEESMGSNSMRSILEEDEE DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRQRDK KASVLYIEGHMNPKMKGFTVSLKSLKHFDCKEKQTLLNQAREDF NQDIGWCVSLITDYRVRLGCGSPAGSPLEYYAADISYPVRKSIQ QDVLGTKLPQLSKGSPEEPVVGCPLGQRQPCRKMLPDRSRAARD RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQYVT CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD VLLPEAIICAISAGDEVDYKTAEEKYIKGPSLSYREKEIFDNQL LEERNRRRR
6486	10	581	LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGRPSGPLHRAWRMMNPRQRMGWIGVGLYLLASAAAFYYVFE ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV IFLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV KASNQISRLQLIDT
6487	352	863	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYSEYL KHNVRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ
6488	878	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDEFFPGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGESLFRGEAYNLFEHNCNTFSNEVAQPLTGRKIPSYITDLP SEVLSTPFGQALRPLLDSIQIQPPOGSSVGRPNGQS
6489	1457	375	KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPAEIREEFERLQRERERRLQQRTNPKGT IGVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQPSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG
6490	3	1183	HEAGCEVWLGVGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6491	3	1183	HEAGCEVWLGVGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIPTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6492	34	2573	IPFLKSCCCCCLPDPPPPPLDQVQEEECEVERVTEHGTPKPPRK FDSVAFGESQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI KRQEVINELPYTERAHVRTLKVLDQVPYQRVSREGILSPSELRK IFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSG PGEEKLKHAAATFCSNQPFALEMIKSRQKKDSRPQTFVQDAESN PLCRRLQLKDIIPTQMQRLTKYPLLLDNIATYTEWPTEREKVKK AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN VEELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL CKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDN KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS TKPIPLPQSTPGEGDNDEEDPSKLKEEQHQISVTGLQSPDRDLG LESTLISSKPQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT EKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP FRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQASNILVMDH MIMTPEMPTMEPEGGLDDSGEHPFDAREAHSDENPSEGDGAVNK EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLQFMTGIP AVESTHQQQHSPQNTHSDGAISPFTPEPLVQQRWGAMEYSCPEI QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTILCQRLAGS ALTDKHSDKS
6493	557	1147	TPARMAYQQSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSKVA KEQNTGHNNINGVVQPSGTSKTLYSTNMALSSSPGISAVQLVRT VGHTTTNHLIPALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIARENH EPERLGLNGIABTTVAMEVT
6494	2425	1052	AVAGGARPCSTPSSPHRRCRHHRPRPLPRPPAAIMSASAVYVLD LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISFIPPDQEFELMSYRLNTHVK PLIWIESVIEKHSHSRIEYMIKAKSQPKRRSTANNVEIHIPVPN DADSPKEKTTVGSVKWVPENSEIVWSIKSPPGGKEYLMRAHFGL PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ
6495	2425	1052	AVAGGARPCSTPSSPHRRCRHHRPRPLPRPPAAIMSASAVYVLD LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISFIPPDQEFELMSYRLNTHVK PLIWIESVIEKHSHSRIEYMIKAKSQPKRRSTANNVEIHIPVPN DADSPKFKTTVGSVKWVPENSEIVWSIKSPPGGKEYLMRAHFGL PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ
6496	247	559	LRAVSLLPLQLVLPEYSIHSLFCIMFLCAQEWLTLGLNVPLLPY HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLI. SFFYYLYCMIYTLVSS
6497	1053	352	ANTQICRLCPRRHLHPPCGARMGNGTEEDYNFVFKVVLIGESGV GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EPGPGEKRACCISL
6498	2636	272	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL LRVSWICGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL AVAVNRTVAHHFPRLLYPTGQRGARAPAGMQVVSHGDERPAWLM SETLRHLHTHPGADYDWPPIMQDDTYVQAPRLAALAGHLSINQD LYLGRAEEFIGAGEQARYCHGGPGYLLSRSLLLRLRPHLDGCRG DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPE KEGSSAFLSAFAVHPVSEGTLMYRLHKRPSALELERAYSEIEQL QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLGWDYFTE QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRF QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARRVSL LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAA NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRY PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPG PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGP DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRD CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST
6499	3	2040	SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETFQVACLP GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRASAEEHLKLAGM ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQPGVFDC LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIATTAHERM PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYALSLIYG KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKADGLIYC LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTE EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINF RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLA SKVEGPPGSTQKAEAACA
6500	1773	726	TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK MLSESSSPLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE TWTKHCDKAEFPSSENVKVFESINMDTNDMWLMMRKAYKYAFDK YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQFFYLGHTIKSG DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ
6501	1	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE IHSRLLDHRPVIQGETRYFVKEFSEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF
6502	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
6503	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVPELNSDSG KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG EVSGPGGSEQSEPNGPGCESSPQPAQLSPQEGPCSCLR
6504	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGPRGPGAGCEMPGRGRCPDCGST ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTPSDEGNLRRVTYSR STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQQAY RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD LDVPSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLPQASPSV PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATPLA WQSLQPADRLSCSLARPCKLANVDLPYPASSRLQELLAVLLRMA EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTAEVET REKEPPGWGQGQGEGEVGNNSLGLPQQKRPASPALLLPPCMLKS PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR QAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHQA ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMQRNASVPNLR GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS ASLTPDPLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSISKASSFA DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE EDISRKGN
6508	862	342	WEARKRPQRWPSERREVRVPPPHLQRGRSGLEPGTFRKMAAARP SLGRVLPGSSVLPLCDMQEKFRINIAYFPQIVSVAARMLKNTTL DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAPLSTSEGL ILQLVGDAVHPQFKEIQKLIKEPAPDSGLIGLPQGGNSLLH
6509	2	1053	FVWNPRGGRKRRRQAAVTQAATRASGTPSPEDGTWTQGKLSVAN KAPGTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELPTTPSWDDQKV RRVPVRKVTTILLIQLLVTLAVVALFTPCDPVKDYVQANPGWYW ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVPTLFLALDTQ LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
6510	37	1156	PCALDGCPQRGAVHFLLSSAMGLLAFLKTQFVLHLLVGFVFVVS GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW SCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERF GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY NQKGMFPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS GSPLLILTFLGFVGAGNGHCR
6511	2541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLE KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV QCEQTDKFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTQEGEQI YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHVSYPCTPTT MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI LLKPKPSQGDSSEAKTPSQ
6512	159	807	PGKKSTWFFLSRSLRVASGRSCKLGHGGYTGSGPGPGEPRDSGA EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
6513	2	756	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAQQESA QAENHLNGKNSSLTLTGETSSAKLPRCRQGGWAGDSVKASKFRR KASEEIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA APPSIQIKRVMTYRDLDNDLMKYSAIQTLDGEIDLKLLTKVLAP EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP AGQARHT
6515	1345	305	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNDIVV VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG AVVALEDDPEPNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLLGGLIVVSK TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
6516	1	1402	FRRLRVLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR KPGIAMKLPEPLSLGNTFNSITLQDEIHDDQGTTVIPQERQLQI LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK ISPQHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK EKFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA INRAPMMGHCHLWYAVLCGYVSEFEGLQNKINYGHLFKEHLDIA IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLPGKIPSSTV QEALHNFLKAEELCPGVSNPNYMYLAKCYTDLEENQNALKFCNL ALLLPTVTKEDKEAQKEMQKIMTSLKR
6517	3	1414	GRVWGGSSSLNAMVYVRGHAEDYERWQRQGARGWDYAHCLPVPR KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAPLEATQQAGVP LTEDMNGFQQEGPGWMDMTIHEGKRWSAACAYLHPALSRTNLKA EAETLVSRVLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLEIYIQQ ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA EKAADIIKGQPALWDKDVPVYKPRTLATQR
6518	242	1098	PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRRHRLLRAVPGPSR RHRCRRRAPPPPSTMGDAGSERSKAPSLPPRCPCGPWQSSKTMN LCSKCFADPQKKQPDDDSAPSTSNSQSDLFSEETTSDNNNTSIT TPTLSPSQQPLPTELNVTSPSKEECGPCTDTAHVSLITPTKRSC GTDSQSENEASPVKRPRLLENTERSEETSRSKQKSRRRCFQCQT KLELVQQELGSCRCGYVFCMLHRLPEQHDCTFDHMGRGREEAIM KMVKLDRKVGRSCQRIGEGCS
6519	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPPGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHILLLPAAAAAASANAKSRRPKEKKEKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ
6520	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPPGKLQLSSRDPPGSLS AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHILLLPAAAAAASANAKSRRPKEKKEKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKHK ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI HIEHQPNGGASVIHCLQ
6521	184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETPPKSKLAEGEEEEKPEPDISSEESVSTVEEQENE TPPATSSEAEQPKGEPENEEKEENKSSEETKKDEKDQSKEKEKK VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITQKGASGTFQLKKSGEKPLLGGSLMEYAILS AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGESKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKP9GGSS KKPATSARKE
6522	1042	392	NKWLRPSPRSHRTPESGRVLSLPRLPPPGMALSGSTPAPCWEED

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECLDVYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA RKRRRPVSPERYSYGTSSSSKRTEGSCRRRRQSSSSANSQQGSP PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF NDTSTCKVVHDLE
6524	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF NDTSTCKVVHDLE
6525	1	1859	GESPFSEEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSSRYK KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT
6526	2	2034	SGRAGEPEEWRGRQYIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESPSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP LQIDHLVPVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLISTGVDVDLQRITLPSINRLRH FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ
6527	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS FIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMETEEVDILMS SDIYSATLSTKSISFTRAQTGWLFREDKTERVGNFLADFYLVNG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LVLESRKRRBHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRQ SLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATIA MSQEFFLGIELLLLNVLEVVAPFKHFNKLREFVQMKLPPGFPVKL DIPVFPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDL
6528	1	1073	LTGPAAAEPRCAADAGMKRALGRRKGVWLRLRKYLFCVLGLYIA IPFLIKLCPGIQAKLIPLNPVRVPYFIDLKKPQDQQLNHTCNYY LQPEEDVTIGVWHTVPAVWWKNAQGKDQMWYEDALAGSHPIILY LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNLVRRLCE RETPPDALILESPFTNIREEAKSHPFSVIYRYFPGFDWFFLDPI TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE PEHQH
6529	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDPDWLF EGVEDESPLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA ALDEALKTCKTSDLKTPRLDDKSLEKLEDEVQTLLKLKNLKIQR RNKCQLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSQE EQSTAALTLYTKKQFFQGIHEVVESSNESQFFNFLKIQTPSICD NQEILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKWAE ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA VVRENAQLLNMPVVKGDFDLQIAKQDYYTARQELVLNQLIKQKA SFELLQLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKQLEML TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELPLTHGN LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL YQQGNQLLLSDQELTEQFHKVESQLNKLNHLLTDILADVKTKRK TLANNKLHQMEREFYVYFLKDEDYLKDIVENLETQSKIKAVSLE D
6530	128	2986	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAQQR INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII SQDLVQVEVLLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPF SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ LLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVPV VHVDEKGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVGPVG YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVFHAH SSVLNPATNRDDPFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSPQEATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFDPPSQDVFTVEPQPFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPPSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSPGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH
6531	845	1425	PSASIPPSASPDDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS
6532	2	954	AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGLYKGVAPPTL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLPSTDFLDGHD LQLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG GAKLCSKLKABLKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES AENLEEVVSVLHVPGYTDTLGEKQTLVVDVVANGGHTWVKAIGR KAEALHNIWLGRGQYGDKSIIEQABDFLQASHQQPVQYSNPHII FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNQ GVKFSVFIHQPRALTESKEALATPLPKDVTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA EKSLQCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS EGASLELRCNYSYGATPYLPWMERTVEEAFILLVCLKPWRVASS LEKKEKEDESFQLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAPLEIDKAFSSHARLS ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHHADDSPLVLTTDGINFMVNSQEIW DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPPGAWGKYKN SEINFSFSRSFASSGRWA
6536	242	1174	SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKPILSIAYSPDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI
6537	1638	921	NRFNPPPTQGPDFSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV FTTYKLMHTHQTVDFVRSKHAQFGGPSYKEMTVMEAVDLLDGLV DESDPDVDFPNSFHAPQTARGIRKAHPDKDWFHLVGLLHDLGKV LALPGEPQWAVVGDTFPVGCRPQASVVPCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLVDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFSKSVEPCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK
6539	218	339	FLGAASPHPHFSSLAPHPDQPEPTPVQDELEAMELWGPGV
6540	3	391	LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVVLDE KQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLP IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEPP RFEGGRKPDSWDGNREPGPGHEHPRDTPRPDHPPHDGHSPASRE RSSSLQGMDMASLPPRKRPWHDGPGTSSHREMEAPGGPSEDRGG KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPGGPPGSGTP SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRVNEGHALYLAFLARKEGT KRGFLSKRTAEASRWHEKNPALYQNVLPYFEGEQSCRPAGMYLL EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE LRCEEEQDGKENMEAIHQASYADILIERBVLMQKYIHLVQIVET EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE DEDPDIKKIKKVQSPMRGWLCRRKWKTIVQDYICSPHAESMRKR NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM LNIYQEPVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQG SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLPTKHFLICTRS SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR YASVERLLERLTDLRFLSIDPLNTFLHTYRIFTTAAVVLGKLSD IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS PAASPPPHTGQIPLDLSRGLSSPEQSPGTVSENVDNPRVDLCNK LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC MKAECFESLSAMELAEQITLLDHVIPRSIPYEEPLGQGWMKLDK NERTPYIMKTSQHPNDMSNLVASQIMNYADVSSRANAIEKWVAV ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAPIEEGT PNFTEEGLVNFSKMRMISHIIREIRQFDQTSYRIDHQPKVAQYL LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	PVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHPVA SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVPHCAVETAKLGP LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNPGIKVPS
6544	630	79	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS EPSDTDPEPRTLNPSPAGWFVQQHPELELMSSFRERPGRNWLQY RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQEEAR GPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMAPLPEAHLG EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAVNGDN CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCPETVYDGY SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
6546	1657	364	HLLNGLDEVAAFPVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS SPGVLKVLAQLGLGPSCANKAEMELVQHIGIPASKIICANPCKQ IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF EEIASVINSALDLYFPEGCGVDIPAELGRYYVTSAPTVAVSIIA KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRRQLMAA EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLAPALCSQPGMHRCCRRRCCCRQPPHALRPLLLLPLVLL PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW NDPHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL RPLA
6548	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAVVPIETDAEDG IKGCGITFTLGKGTEVGELKILSRFQNA
6549	73	1490	ETGRVCEDARPACGSRSRRRRKEAAPGIPTPSPSSSSPTSSRPA ARAFSKAPARLSRPRAREEPPDPGRRYIQEEIIQARKHKLIKMC SSVAAKLWFLTDRRIREDYPQKEILRALKAKCCEEELDFRAVVM DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVQSDSDIT VLRHLEKMGCRLMNRPQAILNCVNKFWTFQELAGHGVPLPDTPS YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSNILGMDVCGIDLL MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASLLPSG RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD PESTERELLTKLPGGLFNMNQLLANEIKLLVD
6550	2293	922	FRVSRDGAPDCGIEQMGLAMEHGGSVARAGGSSRGCWYYLRYFF LFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATERRAEGLYSQ LLGLTASQSNLTKELNFTTRAKDAIMQMWLNARRDLDRINASFR QCQGDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML NQKVKTLEVEIAKEKTICTKDKESVILLNKRVAEEQLVECVKTRE LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD IERVARENSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQ AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVPNFQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG
6551	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAAEVRKNKELKRRASR
6552	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAAEVRKNKELKEEASR
6553	2	1807	FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMPTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSQL EDGGTEYVIATTKLMNGTSWIEALMEKPF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDN KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID LKNQMVLLQGGEALPFSHLILATGSTGPFPGKFNEVSSQQAAIQ AYEDMVRQVQRSRFIVVVGGGSAGVEMAAEIKTEYPEKEVTLIH SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLELPLN EYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	YIMALLRKINQVLLFLLIVTLCVILVKKVHKGTVPKNDADDESE TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG LRNTLTRIRKWIEHSKLRBINFKIVEPNTMGLKGKIRPDSSRPE LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVQGDIQELYDTTLA LGHAAAPSDDCDLPSAQDINRLVQLQNTYMGYLDYRKKAIKDLG ISPSTCSFNPGVIVANMTENKHQRITKQLEKWMQKNVEENLYSS SLGGGVATSPMLIVPHGKYSTINPLWHIRHLGWNPDARYSEHFL QEAKLLHWNQRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFFVTHVLVIILPSLQSFPTFGFLLDIDGVLVRGHRVI PAALKAFRRLVNSQGQLRVPVVFVTNAGNILQHSKAQBLSALLG CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFFRIEGVLLLG EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ STEPVLGGGEPPPHGHRDLCPSPGLMEASHVVNDVNEAVQLVFR KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAVQDRRQQQRLPEWRDPDKYCPSYN KSPQSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWPKESDP SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC QGTNQRQPYFIYPPQIKTEKSGGSIGAADSPENWEKVWDNWRLLT MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG EEAVSKWLDFGEVSTQEALKLIHPTENITPHAVSSVVNNSRNNT PECLAPVDLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKRSKEEEPVAKRP YSQ
6558	21	1138	FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEPAS VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI SEPKTYVDLTNEETTDSTTSKISPSEDTQQENQSMPSLITWNID GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS NYSIITGHEEGYPTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD TQMNSNLGITAACKLRPDRIFFRAAAEEGHIIPRSLDLLGLEKL DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANQTPIAMDCCASRSCSVPTGPATTICSS DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPQPCVPTCP LLNSCQPTPGLSTLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWFRPLPQSCVGTEGGLQVRDTSSRIAKG GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESQLTPC IRNVTSPTRQHHVERKDHSSSRPSSPRPQKASPNGSISSAGNS SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD NTRFVVDPSIFTAQPNTMLGRMFQSGREHNFTRPNEKGEYEVAE GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLVMASAQSGER ECHIVVLTDDDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NRDVAKSVLKERGLKKIRLGIEGVPTYKEKVKKRPGGRPEVIYN YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD QLVVMHPTPQVDELDILPIKPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS PCPMAALTDLSFMYRNFKNCNLVGNLSEKYVFITGCDSGFGNLL AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAEPRVRDVI NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY LPRPADSV
6562	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTEPCVFSGGWL WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKEIFS DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEEE LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE QAAVAPDAVLRPAERQPCPSAQEVQQLRALRAVFRSQQQVRRRR GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLRA HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG TDQEGWQYASDFPASYHGSKIMKDFVRRRCWARKCKLVTSGPWL EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS ELNPAGSSWLHVGTDQPPASISIGACYQVWAVARDGSAFYRGSV YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDENGNLWYRQ GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS SQEQEPSAPPEAHGPVCC
6564	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE KRAAETHFGPETVSBEEKGGKVYQVFESVAKKYDVMNDMMSLGI HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVQSQHQR KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDINKEMLK VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGCKLNGRYISLILAVQIAVLVQAVRAAGKCD AVPKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT VTALTDCQEGAKDMWDKLRKESKNLNIQGSLPELCGSGNGAAGS LLPAFPVLLVSLSAALATWLSF
6566	3	1385	KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAWAQG HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTPFVLTI ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRNRKHGVFV LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW AFVLFYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MHKVPSEGAYDIILPRATANSQVWGSANSTLRAEDMYSAQSHQA ATPPKDGKNSQVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDQDFN YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMQTAESESA MESHSLLNPNLQQGEGVLSSFRTTNQEFVEDLGFWRVLLLIFVI ALLSLGIAYYVSGVLPPVENQPELVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTSLFHPTLASTSSPM LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGSPEYFRNHS LEPLSTFLTYMTCSYMIDNVILLMNGALQKKSVKEILGKCHPLG RPTEMEAVNIAETPSDLFNAILIETPLAPFPQDCMSENALDELN IELLRNKLYKSYLEAPYKPCKNHGDVTAEVMCPILEPEADRRAP IITLNSFGTSLSKEDRETLYPTPGKLYPEGLRLLAQAEDFDQMK NVADHYGVYKPLFEAVGGSGGKTLEDVFYERREVQMNVLAFNRQF HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPQRLGHGRPTPLLCRNRTAGPSHWEKQARAPQGLRPVDPR RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI AEIQKDVEYRLPPTINNLTININILLPPQFPQEKPVISVYPPIR HHLMDKQSVYVTSPLVNNPTMHSDLGKIIQSLLDEFWKNPPVLA PTSTAFPYLYSNPSGMSPYASQGPPFPLPPYPPQEANRSITSLSV ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSQNG FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM KSTPEKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED FLEGKMEIDDFLSSZMEKRTICHCRRAKEEKLQQAIAMHSQPHA PL
6570	330	1304	ARLPRLTPLREGPLVVLLSHWVPVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG LYGLSAVQTMIMNHNTLGYPNVHEITRSTITEMAAAQGLVDARF PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE FICKFCGRHPTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYELAVREETLLL EAFGPCLPDPKSQMEFEAQVFKDPNEFNDW
6572	49	1646	TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDENYCKKLHVQALKNVNSQIRNQMVQNENDNRV QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEEQEKKKQEAYEQLLKEKLMIDEIVRKIYEED QLEKQQKLEKMNANRRYIEEPQKEQALWRKKKREMEEENRKII EFANMQQQREEDRMAKVQENEEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQZEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKZEEENFRKIMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIERE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK
6573	767	275	GGGGGESQSFRAQDGTRTPATDCLMVLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL TRKLSQRPTVEELRERKILIRPSDYVEVADAQDYDRRADKPWTR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKANTA LARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELPEKEPLPP PRKTRAELMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE KWKAERAARLARGEKEEEEEEEEEINIYAVTEEESDEEGSQEKG GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ SEEARRLLGY
6575	117	820	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFPPPPPP ASPERQDGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK LQFEDPIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV AENNEHDVTSTELDPPLTNLSESEMFASELSISLTEEQQQRIER NKQLALERRQAKLP
6576	1	1060	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR GFLLPNLPCVFSSAPTQGWGSRRRWVTPAGRPDFDHLLRTYGDV VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY AGPAGSWSPPHADIFRSFSWSVNVCGRKKWLLFPPGQEEALRDR HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGENVFVPSG WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH G
6577	2271	987	SDRMASDEFDIVIEAMLEAPVKKEEDEQQRKEVKKDYPSNTTSS TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLGELQALRDP AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV
6579	2	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVPVPTSSSVNSSAVT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVQQIGFHRQKDVKIVTVEKKVNEILNRLEKTKVERFPDLAAEK ECRDRBERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVPGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQ AWVQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE KISSSGTAKESPSSMQPQPLETSHKYBSWGPLYIQESGEEQEFA QDPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE ASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL HYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEAAPYQCKDCG KAFSGKGSLIRHYRIHTGEKPYQCNECGKSFSQHAGLSSHQRLH TGEKPYKCKECGKAFNHSSNFNKHHRIHTGEKPYWCHHCGKTFC SKSNLSKHQRVHTGEGEAP
6581	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAIL
6582	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN QHPIIFWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE QQETSTLVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRE ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP PSASVEWCRKCFGAPLI
6583	487	41	RIFSMTSGRLRWRCTWRPATALWSASLRLGTSSMHPSPRSISLP LSMMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGGNWCIF
6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKVNIMAFNAADKVNFAT WNQARLERDLSNKKIYQEEIMPESGAGSEFNRKLRERARRKKYG IVLKEFRPEDQPWLLRVNGKSGRKFKQIKKGGVTENTSYYIFTQ CPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVLNH FSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMS SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKQSDDEAFEDS DDGDPEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQS DSSEESEEEKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSE ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
6585	3	1678	GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAPGVFEVTHDITKYSKAKVPE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILPPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIKASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGADNYYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNPTEVHPDYGSHIQALL DKYNAEKPKNAIHTPVQSGSHLAAREKANL
6586	32	804	PLPEQPAASTSTNPVSGTPAPNKKRKSSKLIMHLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV
6587	75	1117	RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFPNPEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGNIDWAATKLSGLTSTLPDTVLSH LPSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT PLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6588	137	501	LGLQAQLLELRTNNYQLSDSLRKNGVELTSLRQKVAYLDKEFSK AQKALSKSKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA EFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP
6589	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQIWLLLAYCLA CRLLWRLGLPSYLKHASTVAGGFFSLYHFFQLHMVWVVLLSLLC YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSFH LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHQHR LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTBEQGYGMAY TVHKWSELSWAGHWVTFGCWIFYRLIG
6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR RYLEFYVLESKLTEPHGAFPDAQLPSKRIIGPKNYEFLKSKREE FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG KIIKSVPGKLMKEKGQHLEPPFIMNFINSCESPKPKPSRPELTIL SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI VIQELFPELNKVQKEVTSVTSWM
6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR RYLEFYVLESKLTEPHGAFPDAQLPSKRIIGPKNYEFLKSKREE FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG KIIKSVPGKLMKEKGQHLEPPFIMNFINSCESPKPKPSRPELTIL SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI VIQELFPELNKVQKEVTSVTSWM
6592	3	1861	APEFLGSTISSGSMIDANLKLLQEAEQRLKAIVAEKFAIATKEG DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMV LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS MASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEYFMRE TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCL CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN IMHSSLQQGKFDTKGIESTDEAKMSFLVTLNNVEVCSENISTLK KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQ QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR LRL
6593	3	1837	EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLVR RGGEGGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EVYTLDSILPLLNNVHLSHDVYVRRAATENIPVVRRPDRKDLLG YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPRI EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA IKAKIMAKKRSTIKTDLDDDITALKQRSPVDAEVDVTRDIVSRR RVWRTRTTILQSTGKNFSKNIFAILQSVKAREECGRAPEQRVAPN AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGPKIDTMGTYH GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETL IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVPVQ GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKW DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRPRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDLL NLSRKKDPCGQSEINTLKRALBVFKQQVDNVAQCHIQLAQSLRBE ARKMEBPREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNYE QKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK AYMLHIGTLDKVREEWQSEHIKACEAFEAQECSRINFFRNALWL HVNQLSQQCVTSDEMYEQVRKSLEMCSIQRDIEYFVNQRKTGQI PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP NYSLVDDYSLLYQ
6595	57	781	PLGTWSDSDLQEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRKD GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK QQDPSLPLLHTPIPLVSENPQ
6596	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLMVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6597	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIPCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLMVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEWPWQVRFPPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLPNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHQLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS
6599	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAYQSVSAWFEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEANTDLILLNGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILMH RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VVGEQVTSYLTKKPAELRSPNEPKVYMGHGGKPWVSDFSHPHYL AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS ADDGAHSQNEKLNRYNYIEGTKMLAAYLYEVSQLKD
6600	2	934	PGRLPRVAAMESAGLEQLLRELLLPDTERIRRATEQLQIVLRAP AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL QHSTHSPHSPERENGLLLLSVVVTSRPEAPQPHHRELLRLLNET LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMQ TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC GC
6601	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMAVSQPNLVM NHQHQQCMAPSTLSQQNHPTQNPPAGLMSMPNALTTQQQQQQKL RLQRIQMERERIRMRQEELMRQEAALCRQLPMEAETLAPVQAAV NPPTMTPDMRSITNNSSDPFLNGGPYHSREQSTDSGLGLGCYSV PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT NVDLGTLESEDLIPLFNDVESALNKSEPPLTWL
6602	127	617	LLDFPALPKPVLAQSPKAGKPSTWTSMTQSLREVIKAMTKARNF ERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVD NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
6603	79	660	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL SGMGATGTLRTSLDPSLEIYKKMFEVKRREQLLALKNLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD AFSHVVENTAPFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC NQTGVFNQGPHSPILSLM
6604	3	688	TSTAQRQGGERMSFRGGGRGGFNRGGGGGGFNRGGSSNHFRGGG GGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK GPPRGGGRGGRGGGRGGGGRGGGRGGGFRGGRGGGGGGFRGGRG GGFRGRGH
6605	7	848	SGSRRGAMRAAGVGLVDCHCHLSAPDPDRDLDDVLEKAKKANVV ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGEQKEE QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIEVTT QNALKLFPKLRHLLQK
6606	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPABBEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDBEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWNDAGDPSLPIRTPAMIGCSFVVNRKFPGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GPYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISPQGRGGAGPGVPTRTQVFAAMGAVMGTPSSLQTKQRRPSKD KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSVKFE DFVTALSILLNGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA IYDMMGKYTYPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLE SCQEDDNIMRSLQLFQNVM
6608	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS TGTLQLPPQKPFGQEASLPLAGEEELSKGGEQDCALEELCKPLY CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN VVEPAATDVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTPSGQPYC SMCNVGAGEEMEPRQHLESKQHKSKVSEQRYRNEMNLQYV
6609	1	443	FRLRCRRPRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS PATNQAAGQEEKGKAGNVKKAEEEEEIDIDLTAPETEKAALAIQ GKPRRFQKRKKDPSS
6610	319	881	GRKSLCNLHIPIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ VSLRQLEKLFSFLRGYLSGQGSLAETMEQIQRETTIDPEEDLNKL DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS CGWDTESADEF
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSPGVDEEERVRV LQGVRLSENVVNRMKEPSSPPPAPTSSTPGLQDGNLRAPHKEST LPRSGSSGGQQPSGMKECVKRYEQEHAAIQDKLFQVAKRERAAA TKHSKASLPTGEGSISHEEQKSVRLARELESRHAELRRRDTFYK EQLBRIERKNAEMYKLSSEQPHEAASKMESTIKPRRVEPVCSGL QAQILHCYRDRPHEVLLCSDLVKAYQRCVSAAHKG
6612	1724	992	VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM STEAQRVDDSPSTSGGSSDGDQRESVQQEPEREQVQPKKKEGKI SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS TILGPPGSVYEGGVPFLDITFSPDYPFKPPKVTFRTRIYHCNIN SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI ATQYMTNRAEHDRMARQWTKRYAT
6613	130	748	ELELSSNMPEQSNDVRVAVFGAGGVGKSSLVLRFVKGTFRESYI PTVEDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA FILVYSITSRQSLEELKPIYEQICEIKGDVESIPIMLVGNKCDE SPSREVQSSEAEALARTWKCAFMETSAKLNHNVKELFQELLNLE KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
6614	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWEDCR DSRVREKPWRVLPFGTDQFAREALRALHAARENKEEELIDKLE VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVNSF GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT GVTIMQIRPKRPDVGPILKQETVPVPPKSTAKELEAVLSRLGAN MLISVLKNLPESLSNGRQQPMEGATYAPKISAQTSCIKWEEQTS EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
6615	832	35	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYEECQKQGVEY VPACLVHRRRRREDQMDGDGPRPREAPWEPTSSDEGGAASDDSM TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDSKAKPPREKATD EGRRETTVYRGLVQKRGKKQLQSLKKKFKSHHRKPKSFSSCKQS G
6616	347	1886	LLPPCQGARPLSSPPRASEDNLFLFWNCILCAFPHPSPQPLQYP VWPLLLVITQIPAPRHLRNRPPSFSRGGLDSFSGSLSTPSICRS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP PPQPHPCHTCRGLVDSFNKGLERTIRDNPGGGNTAWEEENLSKY KDSETRLVEVLEGVCSKSDPECHRLLELSEELVESWWFHKQQEA PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACP GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD QFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC LDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ IPESAGFFSEMTEDELVVLQQMFPGIIICALATLAAKGDLVFTA IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	118	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP KVCVHHRNPLSLFCEKDQELICGLCGLLGSHQHHPVTPISTVCS RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC LGPATFTFL
6618	548	136	DGKVARRAPNSPAFQNDIYPLVSADRATTAESPWSKVLQNTQCR NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE AFLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA WKYGT
6619	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR YFQRMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG ILSDVQEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE DEPAPAAPLRGRKDEDAFLGDPDTDPDSPLKSARLQRLPSSSSE MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERPRETFLPSG RPPLPGSLLHRPDLAEVLDVLGTSGPAAPYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG
6621	1	662	VQGITSVQQRLQALRKEKSRDAARSRRGKENFEPYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSQSETPEPVVCFPPASDQFLL
6622	2	319	GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRYKVTSMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF
6623	1886	189	KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSPEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLANNEWTPDKL RQKLQTNAHNRLELPLIMLGGLPDTVPEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN LTELELVECDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
6624	218	1786	GSRRGGGSRIPAVSTHVAPGRSVLRPPASGALRLRSLVKALGGC RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPCFHVQSW YDEVKDPSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS ACPPSFGGGCRENLCYKEGSDRYYPPRBBETNEIBRQQSQVHDT HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR QQRKHYFIKSNRNGIQTIGKYQSANSFTVSKVTVQAVTCETTVE QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
6625	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW SFYGQGRKIAEVCCTSIVYATEKKQTKVEFPEARIFEETLNILI YETPRGPDPALLEATGGAAGAGGAGRGEDSENREHRVRRIHVRR HITHDERPHGQQIVFKD
6626	3	1498	SAVEPVYTDRFHLYLGISVEFLCSLRSDATMESITACLRALQAL LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEVV RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEPGEGKDTGGLVP GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED GSRLVSAALVILSELPAVCSPEGSISILPTILYLTLTIGVLRETAV KLPGGQLSSTVAASLQALKGILSSPMARAEKSRTAWTDLLRSAL TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS PGKNSSIQLKTSFL
6627	1	697	GIPHLSSRDNTGTPGAVATRDGEAPERSPPCSPSYDLTGKVHLL GDTGVGKTCFLIQFKDGAPLSGTPIATVGIDFRNKVVTVDGVRV KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE SQKKRSSCCSFM
6628	1	1861	QCAEPGGGSGGGGGSGGGGSGGGRGAGGEENKENERPSAGSKAN KEFGDSLSLEILQIIKESQQQHGLRIGDFQRYRGYCSRRQRRLR KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE EQAVLYNQRVEEISPNIRYCAYNIGDQSAINEIMQMRLRSGGTE GLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF GFRS
6629	5653	4549	GATFLGSVGGRTGKMDAATLTVDTLRFAEFEDFPETSEPDWILG RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLNAFIDR KDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWS SLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGF PAGAEVTNRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP QSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFI PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM TRKTFGFLRFFFSMLQ
6630	2	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMKPKF
6631	2	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMKPKF
6632	1273	568	WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISAIGR GICVLLGISLEDTQKELEHMVRKILNLRVFEDESGKHWSKSVMD KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQAEGFYNSFLEQL RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG DVSSEREP
6633	1145	617	ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSCP VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSPSNENATSNS
6634	1	1134	CGGIPRKGSGPRRRLFMARLRDCLPRLMLTLRSLLFWSLVVYCYC GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF KSEYRVVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD
6635	1420	470	EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVVRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV
6636	1514	1801	SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF
6637	2	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGSWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPNQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSPQESHITVAGWNVLADVRSPGPKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGKRTPPLGPM PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA RLRTASVPLDAVRAEWERTCGPYHKQRLABYYGLYRDLPHGATP VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL PPPFARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIYKKRPVSEAELDERRKRRQEEWEKVRKPE DPEECPEEVYDPRSLYERLQEQKDRKQQEYSEQPKPKNMVRGLD EDETNFLDEVSRQQELIEKQRREEELKELKEYRNNLKKVGISQE NKKEVEKKLTVKPIETKNKPSQAKLLAGAVKHKSSESGNSVKRL KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL GAYSGSSDSESSSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGREIFDS RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM KHMVILFTRKEELEGQSPHDFIADADVGLKSIVKECGNRCCAFS NSKKTSKAEKESQVQELVELIEKNVQCNEKAYFSDDIYKDTEER LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK YDEKIKNIRBEAERNIFKDVFNRIWKMLSEIWHRFLSKCKPYSS
6641	1	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS ASAPPPRGFSAISCTVEGAPASPGKSPAQKSGYPLCLSSLGSLE NPQENVVADIQIVVDKSPLPLQFSPVCDPMDSKASVSKKKRMCV KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGPAIWCKKAK APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHPRPEGKSCSPLAFSAF GDLTIKSLADIEEEYNYGPVVEKTAAARLPPSVS
6642	22	1296	PLEERMMTKNDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNHINPAMDPTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVELEAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDPVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKYKLWDINAITTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	1489	290	FRPLATEPRGSSPVQLVSSTMSVRTLPLLPLNLGGEMLYYLDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEPQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRPVLPVSQPVPWQT EVPQLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM DEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6645	6530	4646	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND RENYDIIKTYHYLYLAMLERPQDGDNILEKEVLPPIHAYGNRTE CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG AVYADNMEPEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLIHLDPRTRE GFTLLHLAVNSNTPVDDPHTNDVCSFPNALVTKLLLDCGAEVNA VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ IPRTLEEPVGFH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLLEL
6648	413	897	RNCWNCPTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPELQKVME KRKRDQVIKQKESEAQKKKSDLEIELLKRQQKLEQLELEKQKLQ EEQENAPEFVKVKGNLRRTGQEVAQAQES
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRRLNEV SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM QLDFQQFLMKLEKLTDIRPIPDKEPVETYIKAYYLTENDMERWI KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
6650	32	765	LVPLVPSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR QKQGSTGEEPHPQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT VKLTEATQLGKDSMERLGKAKPTTRPTAKPTQPGPRPGGNEEAK KKAWEHCWKPFQALCAPLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIPQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG RWKNLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSANIIELLH YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FENNGILVTDVNNFIENISKYAAPFHSSYW
6652	2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPLL PFPLPLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIPFSCSTSFN TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDPYCMYTAYHYV ILVIAPVGSPGDEFCKQRLPQLNSKDNKPLTCTEEDGVLVYHHA QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT CNISVGR
6653	170	1910	FPLEPRLRPFPASRARPVPARTRPSPLHPCCFCPEGGGSMLSPQ RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSPELDEKALASI LLQDHIRDLDVVVVSVAGAFRKGKSFILDPMLRVLYSQKESGHS NWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVPTVEKPGGKKVA VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED DLQQLQLPTEYGRLAMDEIFQKPPQTLMPLVRDWSFPYEYSYGL QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAAA SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT KKMGGKDFSFRYQQELEEEIKELYENPCKHNGSKNVPSTFRTPA VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVQR PSMDKKAQ
6654	1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM WKVTAPIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL PQDLQAARALCVIALLVALPGLLVYLAGAKCTTCVEEKDSKARL VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAQKRELG ASLYLGWAASGLLLLGGGLLCCTCPSGGSQQPSHYMARYSTSAP AISRGPSEYPTKNYV
6655	341	16	KDAYMFKKGLLALVFSLPVFAAEIIWIDVRVPEQYQQEHVQGA INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRNAKVAK DLNPGVKKMSLGQLQSARGVACLGCKGTCSGPEPHSWRKICKSC KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP KEKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM EEPVKQYKSEALGVGEVALPGQGGLPKEEGKQQEKPEGABTTAA TTNGSLSDPSKEVEYVCELCKGAAPPDSPVVYSDRAGYNKQWHP TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT CSKSKRS
6657	830	2120	LLTCQERACDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH HLEAHKNGWANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHPNCSPK LFGDWEAQLRRINKLINGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVQIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPPQYFEK NVQGIVPRSYHWPPPWPVVHLSRQVKYSRLVNDT
6658	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKPSSHRRA SPGLSMPSSSPPIKKYSPPSPGVQPPGVPLSMPPVMAAALSRHG IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSEEMENSSSS MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV SPPQALLQE
6659	18	523	EPQRGDCETWFQNCSLPKFVCFFCWGPWLWRAHSMSNLHSLPGL RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDQRPL NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL VPKLAEELRVGESNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP ESCWYFHQTAIPCLLALAVQASMPEKBPSVLRKVLLEDEVLAAM VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKDGARCC
6662	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC GPKADDGNIFSACAPASSAVKASVSVAQPQQAVIP
6663	3	1005	RPVLSSRVDDFVPPLDETSGRRKKLERMYSVDRVSDDIPIRTWF PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER SPSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAPEDLDWDT EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM GCYILGNPNGEKLFQNLRTLMTPYRVTFESPLELSAQGKQMIET YFDFRLYRLWKSRQHSKLLDFDDVL
6664	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMFPFFDIAHVLVSVMA VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV TRTWKIVGGVTHANSYYENGWIVMIAIGWARGAGGTIITNFERL VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTPQHTQHLAISKHNL MFLYTIFIVATKITMMTTQTSTMTFAPFEDTLSNMLFGWQQPFS SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	LERRLACRQVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL PGRWLGPGCTQNPCSVHTATGPEPRRKLPLLPPDSPNSGYPKEPA ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC PMEMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS ATLIAWELLRTQGLAGLYRGLGATLLRDIPPSIIYFPLFANLNN LGFNELAGKASPAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES SASLPRSPPPTVDESADNAFHLGPLRVTITNIVASTPPTPTCED

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AASRQQRLSALRRYQDKRLLALSNESDSEENVCEVELDTDLPPR PRSPSPEDESSSSSSSSSSEDEEELNERRASTWQRNAMRRRQKT TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST STLEIQPSRASPTSDIESVERKIYKAVKWLRYSYISYSWNKDGE TSLVTGEADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP EGCSKDTPKEETPRTPSNGPQHEHSSSHAWABVPEGTSQDTGNSG SVEHPFETKKLNGKALSSRAEEPPSPPVPKASGSTLNSGSGNCP RTQSDDSEERSLETICANHNNGRLHPRPPHPHNNGQNLGELEVV AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACETPNAGTREDP TDTPATDSSRAVHGHSGLKRQRIELSDTDSENSSSEKKLKT
6667	171	1310	AEEVERLAAMRSDSLVPGTHTFDIRRRSKFANLGRIPKPWKWRK KKSEKFKHTSAALERKISMRQSREELIKRGVLKEIYDKDGELSI SNEEDSLENGQSLSSSQLSLPALSEMEPVPMPRDPCSYEVLQPS DINDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV SYTAQKSGQQQVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL PMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL YTREEEEEEEDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR ELEEKNILPRQTDEERLELRQQIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP LRGNLVKKDCAESCTPSYTLQGQVSSGTSSTQCCQEDLCNEKLH NAAPTRTALAHSALSLGLALSLLAVILAPSL
6669	459	1207	KDEETRKDYDYMLDHPEHYYSHYYHYYSRRLAPKVDVRVVILVS VCAISVFQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQQLLK KAKEKGKVKKSKEEIRDEEENIIKNIIKSKIDIKGGYQKPQICD LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK KKLANDPRWKRYRRWMKNEGPGRLTPVDD
6670	184	594	VARI*GEAAKMSSEPPPPVPGGPTAPLLEEKSGAPPTPGRSSPA VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM PPGPYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA TTVTV
6671	1	763	LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP PEQSRVQPMTASNWTLVMEGENWMLKFYAPWCPSCQQTDDEWEAF AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRR YRGPGIFEDLQNYILEKKKQSVEPLTGWKSPASLTMSGMAGLFS ISGKIWHLHNYFTVCLGIPAWCSYVPFVIATLVPGLSMDLVL*V ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
6672	304	1089	APGSKPVQFMDPEGKTSFGMSVPNLSNAIMGSGILGLAYAMART GVIPPLALLLCIALLSSYSIHLLLTCAGIAGIRAYEQLGQRAPG PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLPF LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ MFHS*LTGVLTQWPIMAFAPVCHPGGAGPSITELCRAFQAQD
6673	1116	1963	LQIQTHHTIHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPND*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRPVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW PGAGHCHSSCDPTRKGAAGGPG
6674	1	440	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ PTPC*IGTRVAFFLT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6675	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE
6676	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLPE KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE
6677	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE
6678	221	865	GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PPPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQQGCHCLVLPAHLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP
6679	2	786	LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSPVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLP
6680	1498	2951	PLCTLPLMPSALPGWAGERWEKQNPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGBARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAENGDQRGGKEEAGEELHRSSSGLTAAPGFP EVHRNLQTPFGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFDSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPFGATEPQVRACGMAPPSPGTSGRLVANGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR FQGGGGG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLPTLHVSERE KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH*LINARLTRYQ TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT YQLSLKFERCLDSEVVTPEILSDDYSKIVPLHNDRYIEPHSQSG FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLPATGTIEGRVECWDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL GPAPRWCSFLDNLTEELEENPESNE
6683	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT YQLSLKFERCLDSEVVTPEILSDDYSKIVPLHNDRYIEPHSQSG FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLPATGTIEGRVECWDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL GPAPRWCSFLDNLTEELEENPESNE
6684	111	527	GLRGGTSRGRAGREPEPAAGVLCVVAGPCQSPCPGGRGREAPA PP\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS RNIVQNYR
6685	258	1473	KLLGDNPEGFCNKPELSDSENGSNS*QSPL\FDRLFDPDPQKVL QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ IFSHCCKGPDHQTILPNHGAVQNIAHLLTSLGYKVRMQALKCFS VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL TASRQGVTST
6686	310	927	DSVTPDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLPKPSLISWLEQEESRTVQRGDPQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVRQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSPH*SIHT
6687	181	915	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSQSST IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVPHKCPDSCWRFKFQPYQLQPYILLSFSSEKPDISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAPISFSLSSVSVGSSAGTTS STSVGSVVAAPTSSSSSSTNRDVAGLDFSTVITSVSQSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLPSPAPLLSKLPTSSGSIAICCQDSGPSDTGRLS VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SSAVIPGYSSSSDSRLNTVPTVDLLCPFQTKSST
6689	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCFSLSS FFSDSISFCFSSSSFCKR*FVSSKVSQNALLSSRLSNGPGGSSK QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNQRF GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSQQGP QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H GDGLAIWYTKDRMQP
6691	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK LEQGEQLWTIED3IHSGACSDIWKVDHVLERLQSESLVNRRKPC HEHDAFENIVHCSKSQFLLSQNHDIFDLRGKSLKSNLTLVNQSK GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSQF ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR CSLCEKAFSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC /GKGFIQKTCLIAHQRFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6694	292	813	SLLLHLAPFGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR EVHSLGQILPQDGLTAEAGPPEAQDPNGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6695	292	813	SLLLHLAPFGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6696	1	782	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRRKFQLCAD LCTQMLEKSPYDQAAMILKARALTEMVYIDEIDVDQEGIAEMML DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKQIKSS
6697	3	782	PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSLKLRNE LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6698	668	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
6699	325	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EGKRIIYNHAFFFQESKWSGGILQ
6700	1098	1392	TQCWRSSTPGMRTHFRTQP/RLECGGGPSQQENGHCMDTNECIQ FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT LLLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRLGI IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ ASAEYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ SPSHSPLKSSBSSSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM VCCEEEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLPYRTCPCSMGLGSSCHLSLPK RAEALLCS3KATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV NNTYRSAQHSQALLQGLLALRDSGILFDVVLVVEGRHIEAHRIL LAASCDYPKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ SPQTELRSDFQCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH PTASLAPRMSNQGIAVLNNFVYLIGGDNNVQQFRAESRCWRYDP RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
6703	45	1244	GVGPRAAAMPLELELCPGRWVGGQHPCFTIAEIGQNHQSDLDVA KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT YGEHKRHLEFSHDQYRELQRYAEEVGIFFFTASGMDEMAVEFLHE LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ VYQIVKPLNPNFCPLQCTSAYPLQPEDVNLRVISHYQKLFPDIP IGYSGHETGIAISVAAVALGAKVLERHITLDKTWKG9DH8ASLE PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNSIQRIAEQE LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK YKQKLKREESVRIKKEAEEAELQKMKAIQREKSNKLEEKKRLQE NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSPT SYKRXGGINSTIAAPYGGKSILITVATGFLGKELMEKLFRTSPD LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVIEKIR AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY PCPVEPKKJIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP EK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6707	2233	1343	YWSGIGYSLQHFHWRKFHFEKKGPPSTCQERLYESRSRWPCIS* GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH TD*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSP*GVARYA C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL ENFTSEAAFIENLRRRFR3NLIYTYIGPVLVSVNPYRDLQIYSR QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAR VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKIIAKG EELL9PLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI LDE\ECLRPGE
6709	3	894	PPHEHLFPSGERGPFSFLVSRRGLGPGKMQKKGKKEKKGRGAEK TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKRQLILF GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCQ\ IPSLPKAASSVYGGYSKQRVKKDVDKGTRHSDMF
6710	158	980	RHKMTNYRVESSSGRAARKMRLALMGPAPIAAIGYIDPGNFATN IQAGASPGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI RDHYPRPVVWFYWVQAEIIAMATDLAEFIGAAIGFKLILGVSLL QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGFVNLAIMATAA SELNFYGHTGVA
6711	3	347	VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHFDTLIHGEFK ELVRTDLHNILMKENKNDQAI*HIMEDLDVTNAHMQIIFKELIML MANLTNSYHDNMHDADYGPGQQHRPG
6712	118	578	PHGQKRTRYPQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRNQDERQYRR PAKLSAPRYMALLMDWIESLI
6713	2485	3	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTPPTSECTSDVE PDTREMVRAQNKKKKKSGGPQSMGLSYPVFKGIMKKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARLPGGHQTVLFSATLPKLLVEFARAGLTEPVL IRLDVDTKLNEQLKTSPFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSPPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL VDSIKNYRSRATIF3INASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS EVVGRKRQRSGPNRGAKRRREEARQRDQSFYIPYRPKDFDSERG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LSISGEDGAPEQQAAGAVLDLNGDEAQNLTRGRQQLKWDRKKKR FVGQSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L GRRRGILTRRRPRTEEVGEARPLAQAGCIPGPHAPRHPLQAESA LELKTKQQILKQRRRAQKAALSLQRNWPQAALCPQ
6714	169	1416	NNCQELLPPPFAPMAHIPSGGAFAAGAAPMGPQYCVCKVELSVS GQNLLDRDVTSKSDPFCVLPTENNGRWIEYDRTETAINNLNPAP SKKFVLDYHFEEVQKLKFALFDQDKSSMRLDEHDFLGQFSCSLG TIVSSKKITRPLLLLNDKPAGKGLITIAAQELSDNRVITLSLAG RRLDKKDLPGKSDPPLEFYKPGDDGKWMLVHRTEVIKYTLDPVW KPFTVPLVSLCDGDMEKPIQVMCYDYDNDGGHDFIGEPQTSVSQ MCEARDSVPLEFECINPKKQRKKKNYKNSGIIILRSCKINRDYS FLDYILGGCQLMFTVGIDPTASNGNPLDPSSSLHYINPMGTNEYL SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEPAINFNP TNPFCSGVDGIAQAYSACLP
6715	32	493	GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP GKPKHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSIHSL PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYPTSPLKKEPS AENVTPWKACERPQQIPASDT
6716	1	176	GAGGPAPRSFGSEEPRAALERDKNSARAAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK
6717	115	896	LPAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG YDYSQQGRPVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN FSDEPPLLEELGINFDHINQKTLTVLHPLKVADGSIMNETDLAG PMVFCLAPGATLLLAGKIQFGYVYGISAIGCLGMPCLLNLMSMT GVSPGCVASVLGYCLLPMILLSSPAVIPSLQGMVGIILTAGIIG WCSFSASKIPISALAMEQQQLLVAYPCALLYGVFALISVF
6718	290	595	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ
6719	1	691	PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG
6720	3	822	HEVAEEAGGTVVPQRGTMPGTKRFQHVIETPEPGKWELTGVEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHQ IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE
6721	3	822	HEVAEEAGGTVVPQRGTMPGTKRFQHVIETPEPGKWELTGVEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAGIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHQ IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE
6722	1	390	RSWSKRTWQALPNAVLPLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWPCSPAAGSFTTLVAQVQVQRPAPDPGK PGHESRLRLLGNYSLNLEGSKEEDAGRYWCAVLQQIMNYQNW
6723	173	659	VCQYCTARWADPGISAGQPVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VEVKELQREPLTPEEVQSVREHLGHESDNL
6724	173	659	VCQYCTARMADPGISAGQFVAVVNDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSABIL AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL VEVKELQREPLTPEEVQSVREHLGHESDNL
6725	356	722	RRRTPPVILATMDDDLMLALRLQEEWNLQEAERDHAQESLSLVD ASWELVDPTPDLQALFVQFNDQFFWGQLEAVEVKWSVRMTLCAG ICSYEGKGGMCSIRLSEPLLKLRPRKDLVEVFFV
6726	98	714	HLQKMERKINRREKEKEYEGKHNSLEDTDQGKNCKSTLMTLNVG GYLYITQKQTLTKYPDTFLEGIVNGKILCPPDADGHYFIDRDGL LFRHVLNPLRNGELLLPEGFRENQLLAQEAEFFQLKGLAEEVKS RWEKEQLTPRETTFLEITDNHDRSQGLRIFCNAPDFISKIKSRI VLVSKSRLDGFPEEPSISSNIIQFKYFIK
6727	1	831	FRGMGDERPHYYGKHGTPQKVDPTFKGPIYNRGCTDIICCVFLL LAIVGYVAVGIIAWTHGDPRKVIYPTDSRGEFCGQKGTKNENKP YLFYFNIVKCASPLVLLEFQCPTPQICVEKCPDRYLTYLNARSS RDFEYYKQFCVPGPKNNKGVAEVLRDGDCPAVLIPSKPLARRCF PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRFLAGIMG RGMIIMGILVLGY
6728	486	935	FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA VIDVDVMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNQPDRRQLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT
6729	259	1191	VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGGPRGRPGYDGCNGTQGDSGPQGPPGSGEGFTGPPGPQG PKGQKGEPYALPKEERDRYRGEPGIPGLVGFQGPPGRPGHVGQM GPVGAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTPHPDQVKGEKGSEGEPGIRGISLKGEE GIM
6730	784	1015	NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF
6731	1	446	GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI
6732	102	1205	GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEPRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW
6733	613	1311	RSCRQVGMRSRNQGGESASDGHISCPKPSTIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE
6734	189	551	SAAMFPVFSGCFQELQEKNKSLELVSPEEVAVHPTWEEWQDLDD AQRTLYRDVMLETYSSLVSLGHCITKPENIFKLEQGAEPWIVBE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELRKKA QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI XDGCT
6736	195	808	MNYELNFKREMPNYKSLGLTNLNFLLKRLSSVLPLITDYVYPEN SSSNPYLIRRIEELNKTASGNVEAKVVCPYRRRDISNTLIMLAD KHAKEIEESESTTVEADLTDKQKHQLKHRELFLSRQYESLPATH IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG EIRVGPRYQADIPEMLLEGTPFCVFAVL
6737	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLEGVRPDTDLS REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIPLSKSQTDV REKRKSLPINHHPPQQIARKYSSCSTIFLDDSTVSQPNLKYTIK CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN PEQKQIYRFVRTLPSAAQLTAECAIVTLVYLERLLTYAEIDICP ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE RQFLELLQFNINVPSSVYAKYYFDLRSLAEANNLSFPLEPLSRE RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL WGAPWTHGRRSNVRVITDENWRELLEGDWMIEPYAPWCPACQNL QPEWESPAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC KDGEPRRYQGPRTKKDFINFISDKEWKSIEPVSGWF
6739	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTNTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTNTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6741	141	960	PLTLPFSSRARAGHTWNTSPGTVGSDPVILATAGVDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILQEGEPFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP
6742	141	960	PLTLPFSSRARAGHTWNTSPGTVGSDPVILATAGVDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILQEGEPFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIPRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELPDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNECHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEEYEAEGQLRFWNP DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CEQVGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL TLALENELLVTKNSIHQACI
6745	1	588	TFRDQGWAQRRRWLLGCASWESWHAAIAAGPGLPSSTARQQNNP AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI RTCQKYIDKYGPLQELEETA
6746	110	492	GATGAMAESAPARRRKRRSTPLTSSTLPSQATEKSSYFQTTEI SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	347	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNL LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQPFKEGDVPC QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGGDGVCPRARGSPQSQQPPSCAGGGEGLQQSGEALDGAM SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQSVSQ INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQLQL HAKTGQSADSGTIKAKLSGPSVEELERELKAN
6750	3	428	SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT TAPGPIHLLELCDQKLMEPLCNMDNKDLVWLEEIQEEAERMFTR EPSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSRRKS RSSQLSSRR
6751	152	1417	PTKATEMAGASVKVAVRVRPPNSREMSRDSKCIIQMSGSTTTIV NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML QHAFEGYNVCIPAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL CDCTIVIGEFQPKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ VKADGPQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV TDTQSPTSDTLLRSTVNGYSEPQLIPLQQLY
6753	2	1305	VPSLPVPPQKVVAHTEPTTSSDSETANGIAKPDPVMPGGEEKAS PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR EERKQARRAKQAEKLSKENVSVSVQPGSSSSVSRAGSLHKSTALP EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE VSKRFSSDDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSYALEKLRE LGFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ FLREMIIQPGIAKANMGVSRSEDVTFEDHPLNPNPDSRWNTYFKD NEVLL
6755	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS LLFEFLPFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL IDYHLAAPITVMLARRLVWALISEATKAGAASMIHYMVLISARL VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL KEQFNNATPIPTHSCPLSPDLIRNEVZCLKADFNHRIKEVLFNS LFSAYYVAFLPLCFVKVSGYLTPMCFLDLCVNYINWVFLV
6756	180	754	IERALGSLPLSIPVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD LRSLQPQPPGLKQSPCLRVLGLQTGATTPGLRDLTCKELIILTE REAQKRKKRKEKESGMALTQGPLTFRDVAIEFSQEEWKSLDPVQ KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE PPHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCNLLFSHLSAVQ TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID PGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ AANQGEFQKPDNKLHQQVLW
6758	1	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCOJGGATK PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK TYHEVVDEIYPKVTHVEPWEKQSRKTAGQTGMCGGVRGVGTGGI VSTAFCLLYKLPTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSPLTKLE WFSTLFPRIPVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQKKTQSGCFDLDSS LLHLKSPSSRSPRPCLNIEDDPDIHEKPFLSSAPPITSLSLLG NFEESVLNYRFDPGIVDGFTAEVGASGAFCPTHLTLPVEVSFY SVSDDNAPSPYMGVITLESLGKRGYRVPPSQTIQVVCVL
6760	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVPQLKDLEKIAPKEKGIT AMSVKEVLQSLVDDGMVDCERIGTSNYYWAPPSKALHARKHKLE VLESQLSEGSQKHASLQKSIEKAKIGRCETEERT
6761	29	1733	ERTLRGLREVAAFSDVADAAVSRRGRCCCCLHCTQTQVAQDCPS SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD RLNFGLARLQARAEGIPVEMVVIGDDSAPTVLKKAGRRGLCGTV LIHKVAGALAEAGVGLEEIAKQVNVVVTKAMGTLGVSLSSCSVPG SKPTFELSADEVELGLGIHGEAGVRRIKNATADEIVKLMLDHMT NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGIIADATVRSLEG RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA AMPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL ERVCSTLLGLEEHLNALDRAAQDGDCGTTHSRAARAIQEWLKEG PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT SLPANSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAWWFMYLLSWLSLFI QVAPITLAVAAGLYYLAELIESYTVATSRIIKYMIWFSTAVLIG LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG LVVVNHYLAFQFFAEEYYPFSEVLAYFTPCLWIIPFAFFVSLSA GENVLPSTMQPGDDVVSNYFTKGKRGK
6763	2	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISR ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYLTELEDGF YLTAFICFLVPILNAGLVWFFPRRRAKPGSTE
6764	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDPR KKWQRTDHELGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
6765	3	550	ARYSRVDHFCRRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL RGSVLVSEALSGSAMDGIVTSVAVGVKRGSDELLSGSVLSSPNS NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTSTE VIALGLPFGKVTNILMLKGKNQAFLELATSEAAITNGNYYSAVT PHLRNQ
6766	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ LQRLKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR IPYGSHIIPPHLCQDLDTAKICVCGRFCLNSPIQGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
6767	336	919	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAARLANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL
6768	2	363	PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAPHL
6769	284	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
6770	1	397	QRNYQVIWSSTNAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGP KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	1	1400	AAAFLQGMTVNGFINTVITSL\ERRVDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDPGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKPLES QFSLSASEAATLFGYLVVPAGGGTPLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG QKVYRDCSCIPQNLSSGFGHATAGKCTST

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6773	1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHPFFQYHRQLYHKCTHKG RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT CVNMPSGPHCLCPQHLTGNHCQKEKCPEPQLLRFFHKNEIWYRT EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGGRCLEVEGHRL CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLTARGGRRAPSPQLWTLVLALIEEKWRSHRILRMNS GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT HMSSCRVDKPSEIVDVGDKVWVKLIGRENKNDRIKVSLSMKVVN QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCARFVHPQWQLLH LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSL TSVAKFVFMAGMMVGGILGGHLSDRFGRRPVLRWCYLQVAIVGT CAALAPTFLIYCSLRFLSGIAAMSLITNTIMLIAEWATHRFQAM GITLGMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIPLTS SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL KSTMKKELEAAQKKKPFLGERLHMPNICKRISLLPPTKFANFMA YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHWGSG RVSSRGRVNCLGLFVLQVW
6777	779	63	CFFHGFAWRDCEVRATFAKKQGQSGIYSCIAFSPAQPLYACGSY GRSLGLYAWDDGSPLALLGGHQGGITHLCFHPDGNRFFSGARKD AELLCWDLRQSGYFLWSLGREVTTNQRIYFDLDPTGQFLVSGST SGAVSVWDTDGPGNDGKPEPVLSPLPQKDCTNGVSLHPSLPLLQ HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC GGGARLQHP**SPRARKGR
6778	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\BETAGDSE/ERSPEEE VQADPRIRSASPKCPTSSPFPKGRSPEGEUET\DPEKVHFHPGP KDKSVAEKN\KGP\SPVSSEGIKDFFSMKPEWENLNQSNVRRMH T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
6779	2	535	RALRRQPRLLAANGIEPESMAISEFIKGSRKFCVNKEELALKKP MAKCAWKGPREPPQDARABASPSGASESDQDQGHESPPKKKAV AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK V
6780	3	403	HEVNDNKPEINTNLMSPGKEEISVIFEGDPIDTPVALVRVQDKD SGLNGEIVCKLHGHGHPKLQKTYRNNYLILTNATLDREKRSEYS LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE K
6781	1	1269	APTRPVPPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL HIPQNIKPSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETGQGLDTTAPGLNGTEQLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASHSLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTPSTVSCKLS NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ NPGELSCKRGDVLVMLKQTENNYLECQKGEDTGRVHLSQMKLIT PLDEHLRSRFNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR I
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQPIPPPRLTPRPNF LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN PQKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT ANCNQGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQPIPPPRLTPRPNF LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN PQKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT ANCNQGEETK
6785	1	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY GAPTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
6786	1820	1397	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSVQSQ INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK YMKSRVEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR EITLKGFREGSPKVLVATNVAARGLDIPEVDLVIQSSPPQDVES YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC ANKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTEEERLQAE WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG RSGGRSGGRSGRQSGSRSGSRQDGRRRSGNRNRSRSGGHKRS FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS SVWN
6787	2646	2270	PSSFPPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI LVPLVEMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLQT
6788	16	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT REGAEDKNTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATQE\ FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEYTAWAMVDGGS NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTPGNQTTIIPAGG AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDICAGNAILKALG GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT GHK
6789	2	678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD PGVFVLLACGTNSSTCGQLASYPLALVRTRMQAQASIEGAPEVT MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI TLGVQSR
6790	2	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD EPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSD HYQWLQVDFGNRKQISAIATQGRYSRSDWVTQYRMLYSDTGRNW KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMXTLKDVI ALNFKTSESEGVILHGEQQQGDYITLRLKKAKLVLSLNLGSNQL GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFR TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG RLNQDLFSVSFQFRTWNPKGLLVFSHFADNLGNVEIDLTESKVG VHINITQTKMSQIDISSSGSGLNDGQWHEVRFLAKENFAILTIDG DEASAVRTNSPLQVKTGEKYFFGGFLNQMNNSSHSVLQPSFQQC MQLIQVDDQLVNLYEVAQRKPGSPANVSIDMCAIIDRCVPNHCE HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL NTPDGSPYTWWVGKANEKHYYWGGSGPQIQKCACGIERNCTDPK YYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKL SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK CLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVR SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD VGAPFEEGMWLRYNFQAPATNARDSSSRVDNAPDQQNSHPDLAQ EEIRFSFSTTKAPCILLYISSPTTDPLAVLVKPTGSLQIRYNLG GTRSPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSY HLPSSSDTLPNSPKSLFLGKVIETGKIDQEIHKYNTPGPTGCLS RVQFNQIAPLKAALRQTNASAHVHIQSELVESNCGASPLTLSPM SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSRQK KPGRRPSMNNDPPTSQRPIDSSKKEWPHLRGGYLAMG
6791	1801	1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW SAVV*SWLTAASTKVQAILLPQPLE*LGLQIAFMASLATHFSNQ NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSMHAVLKLAKGDEVW LRMGNGALHGDHQRFSTFAGFLLFETK
6792	33	1073	VRHTNWGVDMVLPSLGSESPKGAYGHIVSTERTILAVERNKVLL PPLWNRTPSWGPDDPSCCLGSYGSDKVLMTFENLAAWGRCLCAV CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV TCLAASVTFSLLVSGSQDCTCIIWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWXT/VGCEDVCSWTASRRG APGSASKPKRPQVGEEPGLESRAGR*HCFDREAQQNQP\PVTAL AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVPVPPSAVLPMVAPND LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV ASILEGCAFLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP HDPTLKAPTNKGRCHPSPPSTWGSWGL
6794	169	1349	DDVKRRPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\ EPAPPAPAPPEDHPDEEMGPTIDIKSFLKPGEKTYTQRCRLFVG NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA FSQFGPVEKAVVVDDRGRATGKGFVEFAAKPPARKALERCGDG AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR HEEEHRRREEEMIRHREQEELRRQQEGFKPNYMENYVCHFLR
6795	1740	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS DEQRERENEAKLSELRALSIVADD
6796	48	683	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET SVQEGRDCWQR*LPRLFSALVGQPGCWPQGAPPERCV*PGRCKW HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
6797	1620	211	TERMTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSPEASCCK TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS* RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTPTPSS ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART APPPASSAAGAARPAAPSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM ALPEEAKIKDAYHMLKRQG1VQSDPPIPVDRTLIPSPPPRPKNP VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL SNLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF RILFHPAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF RILFHPAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG *PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA RATRARRAVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE NFAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK VKVGKFMAKLAEHMFFKSQE
6801	2	1755	SAESFESQQASVTMHDVDAESPEVLVDYCVTGRVSLSEANVERL YAASDMLQLEYVREACASFLARRLDLTNCTAILKPADAFGHRKL RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDQD YLEGLLTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPNSSSS /R*QQQLSCICSRKSTPETGYVCCQGDGDLLWTPQRSLS\RYDPY SGDIYTMPSPLTSFAHTKIVTSSAVCVSPDHDIYLAAQPRKDLW VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM LCYDPSHNMWLNCASLKRSDPQEACVFNDEIYCICDIPVMKVYN PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITGTTPQWKKNR VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ VAPQRNAQDQQGSL
6802	157	1341	ETFPLFPFLLSKTPGKTASMAHFVQQTSRNIAAESSTEHKECAE PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQNDQQFRSMKELYE RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT RDRLQREKEKEKERLNEELHELKEENKLLKQKNTLANKEKEHYEC EIKRLNKALQDALNIKCSPSEDCLRKSRVEPCHEEMRTEMEVLK QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ IKACQMEKEKLEKQLKQMYCPPCNCGLVFMLQDPWVPTGPGAVQ KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR TPGLK*SSCLWLPKC*NFRPILSKESPSVEVHTNRERQQATRER G
6803	1	2203	KLSGRPVRHMGVLGTSKLVDIRKTIFTFTPQFIDQQQPYLALDN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD QSGEVDFKALVLQLKETSSLQEQADILYNLYTMKGPDWNTELYN ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM SISILTQEIMVYLAMYMRTQPGLFAEMPRLRIGLIIQVMATELA HSLRCSAEEATEGLNNLSPSAMKNLLHHILSGKEPGVERK/SVR PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQSQWQRRRRLDG ALNRVPVGPYQKVWKVLQKCHGLSVEGPVLPSSTTRRMTPGEIK FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
6804	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMTPTKVN GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES LQTVAEEESCSPSVSLEKPPPVNVDSKPIEEKTVEVNDRKAEFP SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK QQKEGKRHK
6805	1539	206	RQPDLKYFGKSFDVSVSESSSLLSNDLPKPADGIKARNRNQNYL VPSPVLRILDHTAPSTEKSADIVICDEECDSPESVNQQTQEESP IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEPNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLISHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHPQEHSCDSQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFPVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT
6806	272	3794	VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GPLLGSCGVPLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVPIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRPLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS AVSQYKARVTPCCYSVMEMCTKGLGAQTGVLRMKGVNLSCVRTC MVVAEERP\RIALTQSFSKLFKDLGLPARAVSTTFGCRVNVAIC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVPTWTNLL VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP INSRGEKQRMHLRDGFLADQLDPIYVAYNM
6807	1444	606	VGHDIVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG SVPQAGPQLQALANLRARRGSIGAALSSRDVSGLPVYAQSGEPR RLTQAQVAAPGENALEHSSDQDTWDSLRSPGPCSPLSSGGQAE SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTEGCLRSLSGDLN RPPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLRDRSR FLFRLPMGLSCPLQVQ
6808	2063	737	GVGSGAASALARSRFLASRLSSRRRTRAPRSGAMQRLAMDLRML SRELSLYLEHQVRVGPGSGVGLSLILGPSVAYAFYYLSSIAKK PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPP\ ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRPTI LLLPGLTGTSKESYILHMIHLSEELGYRCVVPNNRGVAGENLLT PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL GKIGSKTPLMAAATPSVGWNTFACSESLEKPLNWLLPNYYLTTC LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKQN PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH ELS
6809	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP
6810	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP
6811	1522	650	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIPLEDCI VTACQEGFICTWGRPGKVVSFNP
6812	4001	1682	EDAVFSLDLSTIIQGTWPLNGEELKSNEPEGQVEPGALRVRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDPPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDPVVLENEGPHRRLVLPATQPSDGGEFQCVAQDECAYFTVTI TDVSSWIVYPSGKVVVAAVRLERVVLTCELCRDWAEVRWTKDGE EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASPT VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGLEVEESBALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VWSHNGRPVQEG3GLELHA3GPRRVLCIQAAGPAHAGLYTCQSG AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR CEVSPPDADVTWLRNGAVVTPGPQRQESCCSYGGCRMCGQRKART CVSKWRQAEWVQRGPCAGCEVG3PCPTTLACPWPRMGTSTASSS MVSYWPTRAPTAARATTIAPWPGSA
6813	9	836	SSTQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI QRILRNRHDLLNVSQGTVFIPWGPSSYMRRDGKGQVYNNLHLLS QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWP TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC TMYLSHERGRKGSHHRPITEKRVFKNWARTFNIHFFQPDWXPES LAINHPENKPVP
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG TLDNSKSMKPYNYCSAYESJYESTSPECASPQFEGPLSPPPINY NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE DVGPTAEWNGDGSGSLRRSGSPGKLRDALRRSSEMLVKKLQGGT PQEPPNPRMKRASSLNFLNKSVEEPTQPGG
6816	1	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGPLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK
6817	172	3457	LGMMDSFKIGNGLPVIGPGTDIGIYSSLHMVGYLGKNFDSAKVFS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIPMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQPLTPKTEQLKPSRVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLRKKLKASKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEEILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EPNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEPFSSSALNALANDTLDLPHFDEYLPENY
6818	2	240	RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTYTL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
6819	1	961	GIPCTEMGNFDNANVTGEIEFATHYCFKTHSLEYCIKACKNLAY GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ EAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSPVKQCLTLP DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLELTVW DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS PNLNTDMTLVLH
6820	1014	340	GDMVYIVGHVPPGFFEKTQNKAWFREGPNEKYLKVVRKHHRVIA GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN GANNPAIRVFEYDRATLSLKDNVTYFMNLSQANAQGTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS
6823	654	221	PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERPEFYERAXKAFAVVATGETALYGNL ILRKGVLALNPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRC ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLPALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCGS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
6825	3	1173	SSGEFGLQASDIMWTISDTGWILIYLCSLMEPWALGACTPVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLDETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSGGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEMKMSGKAPCAVRHLRDIHLDSPLLSLSP PFGPLALPMDGYGDSLWEEHEYKPCLALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPVIQTLPREYDTP LYFEEDEVRYLQSTQAIHDVPSQYKNTARQYAYPYKVIQTHPHA NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTISEDKS VLKNHDLSVRAKMAIKLRLGEKEILEKAVKSAAVNREYYRQQME EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI RIAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK GSSSDSTAGVKE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6827	1	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPCCRRKRRNL ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNSQHPPALAPPG HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLLLLSLVSGALGL GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVDMLPALFPSS GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
6828	3	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE LGHLSQTASLKRGSSPQSGRDDTWRYKTPHRVAFVEKLTKLVLS QLPNPWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLQSLKGVLE CKPGEASVFQQPKTQEEVCQLSINIMQVPIYCLEQLSTKPDADI DTTHLSVDVSSPDLPGSIHEDPSLTSEQRLLIVLSNCCYLERHT PLNIAEHFEKHNPQGIEKITQVSMASLKELDQRLFENYIELKAD PIVGSLEPGIYAGYPDWKDCLPPTGVRNYLKEALVNIIAVHAEV FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE ICALRDTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN KFKSSMHLQLTCFQAASSTMMKT
6829	1	782	MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR EQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG KLVLDKDMAEEGVLEEAEFYNIGPLIRIIKDRMEEKDYTVTQVP PKIVYRVLQCQEEELTQMVSTMSDGWRFEQLVNIGSSYNYGSED QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEEV EEVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
6830	1	939	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL RYRFPELADPDTCYGPRFCHQLDFSTSGALCVALNKAAAGSAYR CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS
6831	3	1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL EIQSYSLIGHKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI SIPKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNPASKNITKE SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK
6832	1809	412	MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFPEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CPPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSPIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIEVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND
6833	1	1129	PLMTLSQCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDPTSY MEVAKTIKDVFHNHGIHATTIQPEFASVGSKSSVVPCELACRTQ CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSNNLEKKPRRTK AENIPA\VVIEIKN\IPNK\QPESSL
6834	78	1151	AGQERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP CSKLVLSGARGIVGTTVQVLVEAQQPLLLLPTGVWGLNLRAGEE SRAL*LIEEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVEEAQCVEPGQ AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHE LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE QLLRQL
6835	1	834	GIPAADR\EASLELYKLDISRTFPNLCIFQQGCPVHDNLHSILG AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ MAFFRVDHGLMLTYFAAFEVFPEENLPKLFAHFKKNNLTPDIYL IDWIFTLYSKSLPLDLACRIWDVFCRDGEEPLFRTALGILKLPE DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKKWA QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC FRLTPGQFRRTDAL
6836	1	850	MSCGRPPFDVDGMITLKV\DNLTYRTSPDSLRRVPEKYGRVGDV YIPREQHTKAPRGFAFVRFHDRRDAQDAEAAMDGAELDGRELRV QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR RRHRSRSRGPSCSRSRSRSRYRGSRYGSRSPYSRSPYSRSRYSRS PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSSTS SRSASTSKSSSARRSKSSSVSRSRSRSRSSSMTRSPPRVSKRKS KSRSRSKRPPKSPEEEGQMSS
6837	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRGRRKRDS GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS PNVGEFASDEVSTSYANEDSVSSSSDNPQALVKASRSPLVTGSP KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH PGTPGLEQVRTPTSSSGAPPPDEIHPLEILQAQIQLQRQQFSIS EDQPLGLKGGKKGECAVGASGAQNGDSELGSCCSFAVKSAMSTI DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPQNPNS KEAHDLPANKASASQPQSHLQCLSVHCTDDVGDAKARASVPTWR SLHSDISNRFGTFVAALT
6838	16	499	LTDTPPPKTHNIHHSISDYKATLRCWALGFYPMEITLTWQQDEE DQTRDMELVETRPAGDGTPQKWAAVVVPSGEE/Q/RYMCHVQHE GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
6839	1	1195	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG ESLYGDFTEALEHLRHRVIATRSPEIRGGGLLKYCHLLVRGFR PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD AARRYACLVTLHRVVNESTVCLMNHERRQTLDLIAALALQALAE QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAWAYPTWLP CN
6840	4254	2061	ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TDIPVAMEHQPPYIIAVLPRYVEIRTFEFRLLVQSIELQRPRFI TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQPELALQLA BMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF PFDGLLEERALLLGRMGKHEQALFIYVHILKDTRMAEEYCHKHY DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPISSVPSAAVTPLNESLQPLGDVGVGSKNSKRA RERRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFTRVEMARVLME RNQYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG SRPLEFPPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGPSFVRITAL LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAQDMSQVKPVLSKA ERSHIFVWQVSYTPE
6842	3	926	RCQQLSATILTDHQYLERTPLCAILKQKAFQQYRIRAKLRSYKP RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT LSSICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC PPGIKIDAYPWLECFIKSYNVTNGIDNQICYQIFDTTVAEDVI
6843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF SRKSSLIIHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE CNECEKAFSPLSLVTTIFT
6844	244	642	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK I
6845	3	1519	VAVRDECYWRHVPWDQDLWMLLPILMCHPETARARLEYRIRTLD GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV GLAFELYYHTTQDLQLFREAGGWDVVRAVAEPWCSRVEWSPREE KYHLRGVMSPDEYHSGVNNSVYTNVLVQNSLRFAAALAQDLGLP IPSQWLAVADKIKVPFDVEQNPHPEFDGYEPGEVVKQADVVLLG YPVPFSLSPDVRRKNLEIYEAVTSPQGPAMTWSMFAVGWMELKD AVRARGLLDRSFANMAEPPKVWTENADGSGAVNFLTGMGGFLQA VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF SEDSVTVEVTARAGPWAPHLRAELWPSQSRLSLLPGHKVSPPRS AGRIQMSPPKLPQSSSSSEPPGRTFSDVRDPLQSPLWVTLGSSGP TESLTVDPASE*SGTGASEISLGPSLWPRLHPPLLGTLLACHPS PAARLSGKVHAAWPEFKAFCL
6846	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG IIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP MTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK KNPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV RENKTLQRKCADYQINGEIICKCGQAWGTMNVHKGLDLPCLKIR NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
6847	1450	348	SMCWNSDRLEMPLIDLALILVPPSYVPYTGHLSDDSLSRKYCLT WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YPGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE
6848	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH
6849	70	821	SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLVHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKPSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEPAVALGSKLDVINKIGPNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
6850	2	1235	ARGLNHEWTPEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIPSLSNLQELDLKG NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLPKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI
6851	1765	660	VSAQVSAREGENCLGWNLADSSQESVKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA CYCVYKLTIGRDDSEKLEEEGEEEWDDDQELDEEEPDIWFDFET

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSQD INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM YINEVCRETVSRCCNSFLQQAGLNLLISMTVINNMLAKSASDLK FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSPMSL FIRNGNRBILLETPAP
6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTPATLPAVMFAMYIISGLT GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFRBIGTVIDQ IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL KTD
6853	3	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC KCDILKALGIEVDVEDGSVSLQVPVSNEIPNSASSHEEDNRSET ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH VDNPTPEEDETPNQETAVREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYEPSTQAK PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGPCMTGKPG IICVEGFKEHCEEPWHTIRYPNWKHISCKHAESVETEGNGEDLR LPHSFEELLLEAHGDYGLRNDYHMNLGQPLEFLKKHKSEHVFQI LFGIESKSSDS
6855	1913	1148	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
6856	1617	997	VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP HWALFGASERGFDPKDTRHQRKNKSKAISGC
6857	1	617	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGPTFVIYEPWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858	2	669	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN
6859	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSPSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSPRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
6860	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSPVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6861	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MGSPVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862	2	471	EEIDREPHNKLKLKEDXLEKQRKPVNGEDXGDSGVDTQNSEGNA DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNART FGIPLRPNRGRGGYRGRGGLGFRGGRGRGGGRGGTPTAPRGPRG GFRGGRGGREFADPEYRKTTAFGP
6863	2216	487	PQEPALKSEPSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGPLCQNT KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG QVCHNLPGSYRCDCKAGFQRDARGRGCIDVNECWASPGRLCQHT CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS YQCACPEQGYTMIANGRSCKDVDECALGTHNCSEASTCHNIQGS FRCLRFECPPNYVQVSKTKCERTTCHDPLECQNSPARITHYQLN FQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT TFAL
6864	2	2933	LADSSPSNLQIIYKELLSMHHQPDDALTREPDVLPPVDSRSSSG PVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV FYQVQSLFGHLMZSKLQYYVPENFWKIFKMWNKELYVREQQDAY EPFTSLIDQMDEYLKKNGRDQIFKNTFGQIYSDQKICKDCPHRY EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK EKRITVKRTCIKSLPSVLVIHLMRPGFDWESGRSIKYDEQIRFP WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE EFDLNDETLEYECPGGEYRPKVYDQTNPYTDVRRRYWNAYMLPY QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR PHRPNNDRLSILTKLVKKGEKKGLPVEKMPARIYQMVRDENLKF MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ FLPQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRIISALRHMISFLLGASRQNNQIRRWSSAQARREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMPALRELTGSLLALIEMVVYCCPCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHIQQGSESPMMIGEL RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQQSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGVAVPPKLEGIGEGEPLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVPGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS
6866	1571	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKP IIEGMEEAGSVALEELVEKEKDRFPSGVDYIVISDNLWIBQRKP AITYGTRGNSYFMVEVKCRDQDPHSGTPGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLNRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKNP QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAPFL EMAQLH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6867	2833	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP LQSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM HSANDPRSTSCLLKDPPVEAADQP
6868	1	346	RPTRPPTRPEEIKNLYLPYISDMNPVQDLCEDFVELFKTDKGFD KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG GSQGRIVHLSNSFTQTVNCRKPFFSSN
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC VPSLKKDQLPSLSKLPFKSIDHTPMEKFENQLNKFLQNLLSDER LCQSEALYAFLSPSPDYLKVIDVQGKKNSFSLSSPLERLPRDFF SHQEEETEEDSDLSDYGDDVDGRKDALAEPCPMLIGEIFELRGM FKWVRRTLIALVQVTPGRTINKQIRDTVSWIFSEQMLVYYINIF RDAPWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV HLDQLKAGQV
6870	1	1566	MAAVVAATRWWQLLLLVLSAAQMGASGAPQPPNILLLLMDDMGWG DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRQ ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQP QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
6871	209	1126	RMSLNPPIFLKRSEENSSKFVETKQSQTTSIASEDPLQNLCLAS QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPENVPIEQIPLV KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE RLQGLLQVELKTRKTCFWRHQKGKPDTPLSTIRAIYYFLVDYHT DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
6872	880	459	FGLLMVVLSLIFMKGNCVREDLIFNFLPKLGLDVRETNGLFGNT KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG PTSRPPPR
6873	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN IIHTEIPGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKEK DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAEF QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH SSMQNGVKVYNSRRPIS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6874	1	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKNMEKLTS SCPDLPSQTDKKCS
6875	1688	349	VIGTGERGNSASEKWEIMFNEELGDPFYIIHSYSLLNAEEHSYA TLLLRIEKEELDMKGSGFYVSLSWVTISKKNQDNKKYRIIKRDI LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKSDIQIQFLPDHINI VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP CNAQELEECDIFFEESSSLCRPDGNTLKTTHVVNLGSNQYLFSV IVDPKEMPCFCLRHDVDALLWQPHSSKQDDNWEHIATFNALGYV QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI KVNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSHTSVTKLS LHTKPRMPPCDPMPERYQVIPLVNSGSEANELAMLMARAHSNNI DIISFRGAYHGCSPVTLGLTNVGIYKMELPGGTGCQPTMCPDVP RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAPELVRARGGVCIAN EVQTGPGRLGSHFWGFQTHDVLPDIVTMARGIGNGFPMAAVITT PEIAKSLAKCLQHFNTPGGNPMACAIGSAVLEVIKEENLQENSQ EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF AVEVFRSALTQHMERRAK
6877	1	778	GTSPSPARAYAPPTERKRFYQNVSITQQEGGFEINLDHRKLKTP QAKLPTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN PTQRNKDQLIRAAVKPLDTDTICYRVEEPETLVELQRNEWDPII EWAERRYGVBISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	931	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAP EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF II
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK KNSTTDQVYQAIAAKVGNDSTTVNYPALPEVISHSPVRKLAPNE FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF PHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY NEIIFPHCACDSRRKGHVITAISITHPKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVPSHIRLGMGHVLIIVQCPISS MANIYNEKILKEGNQLTESIFIQNSKLVFPGILFNGLTLGLQRS NRDQIKNCGPFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMPH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIPIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESD EDTF
6881	2638	2244	NDSKWEDIHVITGALKMFPRELPEPLPTFNHPNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	1	850	GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRPWLVIN QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KVKATNPRPNIVISGCDVYAEDSNDELLIGDVELKRVMACSRCI LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF VLENPGTIKVGDPVYLLGQ
6883	1794	2256	NSKLKLNQNLKLFITLTVQVLSLHGWGPGIHLQKEGAFPVTQNR ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD ANC
6884	2	99	EFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI KVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR DYKLLDMLQYYLNLTEANLXGESIWKLEYILTQTYDIEDLQPES LYGLAKQFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA IMNLDNISYADCLKQLYIKHNY
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRPGPNSS LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR KVVLNQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG GQQRAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAPLTG TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT FASNNVTDMFPDLPPTDELRQRYCLDTWGVWPRPDWLLTSFWGG DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL SL
6888	1	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH IFEMYEEINQFLFHKSSNLVDGFENKEPKIHLAYLADLFKHLNE LSASMQRTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL EEIIVSDNEGIFIAAEITLHLQQLSNFPHGYFSIGDLNEASKWI LDPFLPNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC AQFTAFPNLAKTALEILMPPATTYLCELGFSITFTPQNKVPEAA LILSDDIRVAISKKVPSFLGHH
6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL WKAESISLDPGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVDKIREFLQKISKEQGLEVLPEHDPIR DQSWYVNKKLRQRLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF TGPLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV ALQSFTSHLLGDAGSPYLIGPIGDLIRQSTKDSPLWEFLSLGYA LMLCPFVVVLGGMFFLATALPFVSDRARAEQQVNQLAMPPASVK V
6891	1980	1262	LRIHQELLSKELKLLRGITIESIYIHIGLAAGKEQPMQDASNVMQ LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE AVPLLVKVIKRAHSKTKQNVIATENCISAIGKILKPKPNCVNVD EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC VSQLDDEQQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH QPVAIELWKAVKRHNLTKRWLMKIVDERREKNLDDKAYRNIKELE NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYIDIA SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDPLKKIQRVDFD IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG RTVTIKLKNVNFEVKTRASTVSSVVSTAEEIFAIAKELLKTEID ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS ATECTLEKTDKDKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE NVPASSLCEKQDYEAH
6894	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS VFNPW
6895	2379	478	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS MNFTPPQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL SIPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV PPPRGRGRGGFGQGGIRPIDIFRQRKQNTSRPPSMHVDDFVAAES KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF PTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSQSGGSRG KFVSGGSGRGRHVRSFTR
6896	1	555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS FAVYAATATEKSEWNMHINKCVTDLLSKSGKTPSNEHAAVWVPD SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERDWETAIQKPLCSLPAGSGNALAASLNHY AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL SLANGFIADVDLESEKYRRLGEMRFTLQTFLRLAALRTYRGRLA YLPVGRVGSKTPASPVVVQQQPVDAHLVLEEPVPSHWTVVPDE DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEFKDGKGVFAVDGE LMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL
6898	919	346	QKTVTAVASLLKGRQGIYTENERRMGAVIKIRPFFKIMLVLIICW LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTWFINGILNPA QGFLLSLAFYGWTGCSLGFQSPRKEIQWESLTTSAAEGAHPSPL MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIEIHTASESC NKNEGDPALPTHQDL
6899	120	827	MKVRKNNDAYLLDKNKINMDCFISCFFKKMLTTLMFSHSGILSL LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS NGETKYVDLTKLAVTKKRVRPLEKQDPFESRRLWKNVTDSLRES EIDKATEHKHTLSERQRTEERHRTETGTPWKTKYFIKEGDGWVY HKPLWKIIPTTQPAE
6900	3	451	TEVLGSKGIHELRSSTSALHHALEESASLLTMPWRAALPSTHIP VLPGKVGESTERELLELRTKVSQQEQLLQSTTEHLKNANQQKES MEQFIVSQLTRTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP LADLVGDSWPALRFQEK
6901	1	201	DDNNVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP SFPKAARQFLLKNSFYRYHLGFS
6902	2	267	GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGCAGAQGA SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLFENN
6903	1	149	RINQVYRQSPTGIHILVIDQMVQNFQDESCFLPSTVKAESSDGI HIILK
6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILPNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNPGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQPFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWPCLASPEVEKHLVVNIGTH CVLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RKFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQILELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD
6905	1	226	VSKTGEAETITSHYLFALGVYRTLVLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA
6906	3	611	SVDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVPTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD
6907	2	2228	LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAQSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLQSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPQQIQAVRDDVESQFPA WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGKS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AREAAASLSLTLQKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA DYALESGGASVISTRCSETYETKTALLSLPGIPLWYHSQSPRVI LQPDVHPGNCWAPQQPQGFAVVRLSARIRPTAVTLEHVPKALSP NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGEPIQTFHP QAPTMATYQVVELRILTNWGHPEYTCIYRPRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG PQGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV GSALATPCSSARRAHLKYTTFKAGPILELEQWIDKYTSQLPPLT AFILPSGGKISSALHFCRAVCRRAERRVVPLVQMGETDANVAKP LNRLSDYLPTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAPSDYP SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS LYC
6910	1	1068	LVPVVVIESVYVGKLVIADLNIVLYNIPTPHGPDLYGTEPWYPY LINGFLNFNVAPALALLVLPLTSLMEYLLQRPIHVQNLGHPYWLT LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLPGLLSFSRSVA LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF PSSFLLPCNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK KSGG
6911	1184	966	GEDAEEMETGNVANLYSIPGSSFSGLLRKGPGGGREEEEGEESG PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSPQMLFTYLSTGSALKAQSYEDAYRCIKSSILLGSI SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSRIYNIVESFEEVE DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL SARHVPSLILETKGIPVTLNGKKVEVAVKQIIAGKAVEQGGAPS NPETLDLYRDIPSLQGF
6913	1643	1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDI CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR QELREAQTHIRATCISPGVVETQFAPKLHDKDPEKAAATYEQMK CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD VAFITTVTPLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD VAFITTVTPLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT ALILTELLMVALTVRTWHNLMVVAEFLSLGCYVSSLAFLNEYFD VAFITTVTPLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSPPQWLPGGGGGQVSSCS DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLQSP VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLAN LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGE VFTQAMPLRKPGGPFYVPESFPEGGYPAYASGGGYVIAGRLAPW LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6919	850	41	QGRRELSGSVFCPFIQQEPKEMLTLSEYHERVRSQGQQLQQLQA ELDXLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEPHVFPG NCNAFEGDQGQVVIQLPGRVQLSDITLQHPPPSVEHTGGANSAP RDFAVFPLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEIQTFHL QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS AQGPH
6920	1418	591	EAQGPSKVHLTLKKKK
6921	2	1711	MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP SNCLGIRSFGDAQGCTELLNVAHKYTMEHPIEVIKNQEFLLLPA NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS YIRLPLLPPQLLADLETSSMFTGDLECQKLLMEAMKYHLLPERR SMMQSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY PDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC SRLSDCVERYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP
6922	1075	369	LTPPAGIRHEVRDRERERER

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLPRKSLNVGLHYSHIPFLT TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS LPSPLPNLGPQQPALTPEQENILHTTQTDCYNNLAACLLQMEPV NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
6937	1	727	AVEFRCCPGRDPACFARGWRLDRVVGTCFCDQACRFTGDCCFDV DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA TSPHWSTHTEDAGYCMEPKTESLTPHCALENRPLTRWMQYLREG YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVDTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA TGLQRRRLIPAPLFDTTALGRKPSLPGQWVDLPPPLAGSLKEPF EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ EVDV
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV LADSVHLAWDLSRSLGAVVFSRVTNNVVLRAPFLVGIEGSLKGS TYNLLFCGSCGIPVGFHLVSTHAALAALRGHFCLSSDKMVCYLL KTKAIVNASEMDIQNVPLSEKIAELXEKIVLTHNRLKSLMKILS EVTPDQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLAIAEAQRQAEALGYQA VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL HELAAELQIPDLQLEEALSTMAWGRGPVCLLAGGEPTVQLQGSG RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDQDGPTEAAG AWVTPELASQAAAEGLDIATFLAHNDSHTFPCCLQGGAHLLHTG MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6943	1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG TKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQKY NSGVTMGCWGMCIYAPSAAFYSAILEKLEEFLSVRTLYFIAYLA FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDVYQ SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLL LNV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC HSKPGPARPVPLKKRGYDVTRNPHLNKGMAPTLEERLQLGIHGL IPPCFLSQDVQLLRIMRYYERQQSDLDKYIILMTLQDRNEKLFY RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK AYDDLLDEFMQAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQQAGEAAM G\IAHLLVMALE\KEGVPKA\EATRKIN\MVDF\KGLIVQGRDH LNHEKEMFAQD\HPEVNSLSEVVRLVKPTAIIGVAAIAEA\FTE QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF PAS\GSPF*GVLIWEMGKTPIPGGRGNNA*RVPRGWQLGVHSPQ GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR NVFLRIAIKVFD*GYKHNLV\GYYPEPKD\KEAPCKIPGSYTPD VDSFYT/VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC NF\EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG C\TNILLLRKENPGGL/CEDEYLFNPTCQVLVKDPTFEGFSRLR F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ. WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLFDIARIE RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEP QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA VGKNGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD NCEMFLNFNGNKLFLDCLNEFPEKQELIRNMLGLLGNVAEVKEL RPQLMTSQFISVFSNLLESKADGIEVSYNACQVLSHIMPDGPEA WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPILRLLPQ GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM ATARQETKEMARKVIEHCSNFKEENMDTSR
6947	2	1682	TSVSTIPRGLASARPQSRSWRCCPVWRRSPGRARGRGLKWNLNVP SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG LKGRLIEVTEEELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLK DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVTI /EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDPLGHPLKNHNSL IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK IYPTGLPTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLLA AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE KLAPKDKRLDVEFVLSAPISEWNGKQGHISPALLSEFLKRNLDK SKVLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
6948	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSR CRYSHQVDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT DGFLKDNNNAAQRLLDGMNFMAQSVSSLSLGPTKAVTSWLTDQI APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT QETVE
6949	152	4656	GLRICLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT EEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS SAFPIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAPGTLSP SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA PVRRQMKAKQLSAQSYGVTSSTARRILQSLESKMSSPLADAKRIP SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTFNPSSPEITTSSPSPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTP SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNPKPGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESSKPEEVKKDSKNDNPKFGLSFGL SNPVFLTPFQPGVSNLGQEEKKEELLKSSCAGPRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSPGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVPGEG KLTMKEPKC\QPVFSPGEFQRQTKDENSSKSTPSFSMTKPSEKE SEQPAKATFAPGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGPGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQP NPPGFGSISSSTALPFTGSQPAPPTFGTVSSSSQPPVFGQQPSQ SAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTP AASAQPSGSGGFPFNQSPAAPTVGSNGKNVFSSSGTSFSGRKIK TAVRRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDELHYQDTDS DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQQDWKFLASHPPNR TDQQCQYRWLRVLNPDLVKGPWTKSEDQKVIELVKKYGTKQWTL IAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDRIICEAHKV LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN SEEELAAATTSKEQEPIGTDLDAVRTPEPLEEPPKREDQEGSPP ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRQRR RRVALSPVTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF WNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE VLRSEAGIELIIEDDIRPEKQKRKPGLRRSPIKKVRKSLALDIV DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE KARQLLGRLKPSHTSRTLILS
6951	1940	239	AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT TSSKPEGRPRGQAAPTILLTKPPQATSRPTTAPPRTTTRRPPRP PGSSRKGAGNSSRPVPPAPGGHSRSKEGQRGRNPSSTPLGQKRP LGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQTVAAT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGGSTPTSQGGTPDA TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYP\CT SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQQASTTPQAP THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIG STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S WPSACPSPP\LCPADGVLHEEEEEDRQPQEQPEAYGNNTHHPGT TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGNVP C
6952	658	304	PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT ASRQARGELRLCLTTAVRGTSPSVSPVCQSS
6953	1512	349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM\CPVC GRALSSPGSLGRHLLIHSEDQRSNCAVCGARFTSHATPNSEKLP EVLWMESLPTVHNEGPSSAEGKDIAFSPPVYPAGILLVCNNCAA YRKLLEAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDN ETPEEREVRRMRDREAKRLQRMQETDEQRARRLQRDRBAMRLKR AIETPEKRQARLIRERENKRLKRRLEKMDMMLRAQPGQDPSAMA ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH
6954	819	1	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQN *PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRLP PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRTR *CAGAAARGRPRRDRSPRPRTPGGCSWSEPRTPPAVSASAQTPS DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHPR AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGGAPFNQVGSS VMQAMSTGI
6955	1968	782	PPGRRQVRAQVAGAPVGHWGTRAHQVKTGGRRRARRTMPFLGQD WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSED GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK ERHGYCTLGEAFNRLDPSSAIQDIRRFNYVVKLLQLIAKSQLTS LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCIL /N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQLW KKLCQYHPAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQY GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK F
6956	8605	3839	QTSTSIFASPTSPPVLGESVLQDNSPDLNNGSDAEQEEMETQSS DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAAS PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTASV TSPKASPVTSPAAAFPTASPANKDVSSPLETTADVEEITGEGLT ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGETW YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDFF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI AKSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKKS KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKAD KTLATQRRLEERQRQQMILEEMKKPTEDMCLTDHQPLPDPSRVP GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEGL LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSKI PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQKAAV LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLRRLKT VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEEEEEEESI AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLPFRKKLLH SSQMLRAVSLGQDRYRRRYWVLPYLAGIPVEGTEGNLVPEEVIK KETDSLKVAAHASLNPALPSMKMELAGSNTTASSPARARGRPRK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ LQLQSHKQFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS PVQPSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF FKQMEQRYLTQLTAQPVPPEMCSGNWWIRDPEMLDAMLKALHPR GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM SWSPKEKTYETDLAVLQNVEELEQRVIMSDLQIRGWTCPSPDST REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTRIS YEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT CLVCRKGDNDEPLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTPCEIILMEME SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRPFE\SRWEEF YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV RYNPDF	
6957	82	3514	MLIVAMPEPTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV ETPPGEEQAKQNANSQLSILPIEKPQGGTVKVGEDITFIAKVKA EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERHSRVYTFEMQ IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL EDTTDYCGERVELECEVSEDDAQVKWFKNGEEIILVQTRYRIRV EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDGKAIMEG SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIFAVNA\I GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD LIDKTKPTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFPQGKPRPELTWKKD GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT GYTIQKADKKSMENLRVIEHIIEPVPHTELVIGNEYYFRVFSEN MCGLSEDATWTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS NQGVCTLEIRKPSPVDGGTYCCKAVNDLGTVEIECKLEVKVIAQ	
6958	274	1663	PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTEPLSL DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR HLANIVERVKEVKMSPQEGQKRDVCEHHGKKLQIFCKEDGKVIC WVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAEK LEDDIRQERTAWKNYIQIERQKILKGFNEMRVILDNEEQRBLQK LEEGEVNVLDNLAAAATDQLVQQRQDASTLISDLQRRLRGSSVEM LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE LTDVQYYWVDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK RKSSGFAFDPSVNYSKVYSYRYRPQYGYWVIGLQNTCEYNAFEDS SSSDPKVLTLFMAV\LPVVLGFS	
6959	1	1469	SLVHVVEFGRGIBDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQPQTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWLPPNVT WTELEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFIGLPLS RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCGL TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFVGGLSV LYHESWLWADVMCWDRYFNQLTLSCPAADSEA\SLYWWYLLSLG FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVIH HFVAVILMTPSYSANLLRIGSLVLLLHDSSDYLLEACKMVNYMQ YQQVCDALFLIPSFVFFYTRLVLFPTQILYTTYYESISNRGPPF GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMFKDIRSDV EESDSSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN RHTTAT	
6960	387	2068	AKWAREKEMQEP\TRSPF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPEEKQALKRLVSEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFRFNSESESGSEASSPDYPGPPAKNGVASRSHTHP KEENPRRA\SKAVESSSDEERQRDLPAQRGEESSSEEEEKGYKGK TRKKPVVKKQAPGKASVSRKQARESESESEAEPVQRTAKKVEGN KGTKSLKESEQESEEEILAQKKEQREEEVEEEEKEEDEEKGDWK PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKSAASSG DDSGRDREPPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGBPTA KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGE LYRRTLDSDEERPRAPPDWSHMRGIISSDGESN	
6961	340	1646	RPWSSPTMKPNPSLRLRIFNLNCWGIPVLSKHRADRMRRLGDPL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPPGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARREAQDLGPEPQLYALL\LGQQEGDRTKEQ	
6962	340	1646	RPWSSPTMKPNPSLRLRIFNLNCWGIPVLSKHRADRMRRLGDPL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPPGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARREAQDLGPEPQLYALL\LGQQEGDRTKEQ	
6963	374	2618	RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNP EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVPPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESPDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR QTETLTSNLRMPLTLTSNTQVIGTAQNTYLPALPTTQPAGSGPK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPLASSAGH STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNKRFTQKSSLNVHM RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTPPAGTPP GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMRMHVSDG
6964	1	178	SGRPPFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL QIFIG\NCSMFVLVI
6965	757	208	NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISPFLCLKDRSDFRP PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\CCMEHDL PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGSTLALRRY FQESISTLE
6966	820	1867	IITALGVRGMPGCPCPGCGMAGPRLLPLTALALELLGRAGGSQP ALRSRGTATACRLDNKESESWGALLSGERLDTWICSLLGSLMVG LSGVFPLLVIPLEMGTMLRSEAGAWRLKQLLSFALGGLLGNVFL HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVIAGILTFLALEK /HVPGQQGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR GP\DIKVSGYLNLLANTIDNFTHGLAVAASPLVSKKIGLLTTMA ILLIEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGPA ICTQSPKGVEETAAWVLPFTSGGFLYIALVNVLPDLLEEEDPW
6967	162	633	GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEEGSELNGFEG TDMKDMRLEAEAVVNDVLFAVNNMPVSKSLRCADDVAYINVETK ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\ SPAYREAFGKR\LLQRLEALKRDGQS
6968	1	2265	RGGGGGRGGPGARERERPGEPERTMEAAAGGRGCFQPHPGLQKT LEQFHLSSMSSLGGPAAPSARWAQEAYKKESAKEAGAAAVPAPV PAATEPPPVLHLPAIQPPPPPVLPGPPFPMPSDRSTERCETVLEGE TISCFVVGGEKRLCLPQILNSVLRDFSLQQINAVCDELHIYCSR CTADQLEILKVMGILPFSAPSCGLITKTDAERLCNALLYGGAYP PPCKKELAASLALGLELSERSVRVYHE\CPGKCKGL\LVPELYS SPSAACIQCLD\CRLMYPPHKFVVHSHKALRNRTCHWGF\DSA\ NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP RVSSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS LGCVHPRQRLSAFRPWSPAVSASSKELSPHLPALIRDSFYSYKS FETAVAPNVALAPPAQQKVVSSPPCAAAVSRAPEPLATCTQPRK RKLTVDTPGAPETLAPVAAPEEDKDSEAEVEVESREEPTSSLSS LSSPSPTSSSSAKDLGSPGARALPSAVPDAAAPADAPSGLEAEL EHLRQALEGGLDTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKNKEA NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL QHAEADREQLRADLLRREAREHLEK\VVR\ELQEQLWPRARPE AAGSEQ\AAELEP
6969	1855	118	AGTNHGRLKVRTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQA GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR NFSNYSSWHYRSCLLPQLHPQPDSGPQQGRLPEDVLLKELELVQN AFFTDPNDQSAWFYHRWLLGRADPQDALRCLWVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKNCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL PSVSSVLT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6970	3	1528	SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE GPLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPPPA QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS KSTYSLTRRISSLESRRPSSPLIDIKPIEFGVLSAKKEPIQPSV LRRTYNPDDYPRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI QLVHGLKLVKTKKTSFLRGTIDPFYNESPSFKVPQEELENASLV FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT AVEQWHSLRSRAECDRVSPASLEVT
6971	37	3702	ACFYVPGSRSFKLYPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS SDSNPAICHRRQAARSRFPSRPSGRSDLTVDAVKLHNELQSGSL RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTPSKVQ RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA AQHGVCSVLKGSEFMPEKAPAHHPAAISTAKFCIQEIEKSGGSK EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA CAMQAPHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV EEGLTYKFHAAWSSVLQLLCVFPEACGRQAHPVMRKCLQSLCDL RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG STVESKIYDTLQNQMWTLLPGFCTRPTDVAISFKGLARTLGMAI SERPDLRVTVCQALRTLITXGCQAEADRAEVSRFAKNFLPILFN LYGQPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK AHGVQKKAYRVLEEVCASPQGPGALPVQSHLEDLKKTLLDSLRS TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTREVSV GARKNAPALLVEMGHAFLRFGSNQEEALQCYLVLIYPGLVGAVT MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRIIFRMK LRNLFT\KFIPR\FGILTWGKKAVGPKEYHRVLVNIRKAEARAK RHRALSQAAVEEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE EEERSRGKEQRKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA TQPGPGRGRKKDHSFKVSADGRLIIREEADGNKMBEEEQAKGED EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYQAGGSGI HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR RKKMKLQGQPKGLVKAAQRGSQVGHKNRRKDRRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSFS PAEAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA AAATERARRGATMGAQLSTLGHMVLPPVWFLYSLLMKLFQRSTP AITLESPDIKYPLRLIDRIIISHDTRRRFRFALPSPQHILGLPVG QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF ANQTEKDILLRPELEELRNKHSARFKLWYTLDRAPEAWDYQGQ\ FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DIIVGH PTERCPVF
6973	1	1964	LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA SPRRQEILSNAGLRPEVVPSKFKEKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILSKPVDKQDAY RMLSRPE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDPL NVVGPPLNHFCKQLVKLVYPPRPEDLRRSVKHDSIPAADTPEDL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SDVEGGGSEPTQRDAGSRDEKAEAGEAGQATAEAECHRTRETLP PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPQKAADIAS KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE YSLHGFIMHNNDLTWNLFTYLEFAIREGTNQHHRALGKKAEDLF QDAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFQPPGPQAVQ IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAQAACSL
6974	3082	2172	RSCAAFASFASRPPLELPAPPGSHRSPPGRGVATSAQCALSVRK LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV SLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNNSVLPVTASAP TSLLPKNISIESRREEITSPGSNWEGTNTDPSPGPSSTSGGVH LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSL STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESPTEESSSDHT PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVPHAHSGKEGDKYKLSKKEL KELLQTELSGPLDVKELML*ATEALKTPEEA*KSPIIQCSSSRS SLPPAPQPPPYL*LSAVPFPIHLPLPLLPPQAQKDVDAVDKVMK ELDENGDGEVDFQEYVVLVAALTVACNNFFWENS
6976	1216	970	GCQL*VAYGTTENSPVTFAHFPEDTVEQKAESVGRIMPHTEARI MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKW YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFPHTH PKVQEVQVVGVKDDRMGEEICACIRLKDGEETTVEEIKAPCKGK ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGNRTVEPFPEGTQMAVPGMGCFNGAERKFWVLKG VYSTQVGPAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KENYQKVLSEHGPGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK
6978	3	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAAILSRCRHWSGPPPPPPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMXQGAPTSFLPPEASQLKP DRQQPQSRKRPYEENRGRGYPEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSPTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNP GQRAEPYCSVLPGFTPIQHLPLSERIRGTVGPKSKAECBILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPPQPPPQQPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSPGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYCQYAQQWNQYYQNQGQNPPYYGNYDYGSYSGNTQGGTSTQ
6980	1	420	GTRGRKTGRVAAPSTRRRTGNMQKLQTRSPAMSLSDPGLGYHPT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CWTLRWPPLCSLHALHVPHCLPSSRLGTPVSPRLANDPNCSCEA GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA SEKCSCCA
6981	10	1054	PGRGPRRASLRDAPAARGVFQGGLGQAKQARTRACAALPTPHPS APRLLEPQGVPSLPPPPPGPWPNMILTKAQYDEIAQCLVSVPPT RQSLRKLKQRPPSQSQATLLSIFSQEYQKHIKRTHAKHHTSBAI ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERPLQ EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQPWSYWNRPG PGLVIYWYGPIQELDCNRERGILLKACPPTNIVTLCHSIA
6982	153	1285	FPQQDCSAPAAPGLAGSEPRHLRAYRRRRQRARGLKRVAWLAPP PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV GDTVETLMLHPVIKAPLCGSISGTCSTLLFQPLDLLKTRLQTLQ PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCNSPITVI KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPP SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIFAGILASLVT QPADVIKTHMQLYPLKFQWIGQAVTLIPKDYGLRGFFQGGIPRA LRRTLMAAAMANTVYEEMMAKMGLKG
6983	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVPLSKPQK AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDPQPYFKGE IFLDEKKKPYGPQRRKMMFMGFIRLGVWYNPFRAWNGGFSGNLE GEGFILGGVPVVGSGKQGILLEHREKEPGDKVNLLSVLEAAKMI KPQTLASEKK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIPYDMKVR KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT DPFKHFVGMLPEKDCRYALYDASFETKESRKEEIMFFLWAPELA PLKSKMIYASSKDAIKKKPQGIKHECQANGPEDLNRACIAEKLG GSLIVAPEGCPV
6985	1887	1324	RRTAGIVPCFPKPGRTRHALCSVVLLLLTGQLAFDDFCESCAMM WQKYAGSRRSMPLGARILPHGVPYAGGFAIVYYLIQKFHSRALY YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK LSGENGDEVKKE
6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDPRNVIAF VPKEKKKKSALFEVSEVIPVMTNNYEENILKQVRDSSYSLESSL ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC LLFSRWKESDEPFRPVQAKFEPHHGDYEKQFLHVLSRKDKTGIV VNNPNQSVPLFIDRQHLQTPKNKATIPKLCSICLYLPQEQLTHW AVGTIEDHLRPYMPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNVETENWSPQKSQRRYDMYNTAC FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP DPRNECYLALSKFTSHLKNLQSDLKRCFDPFIDYMVLLKMRYTQ KEIAEIMLSKKVSRCFRKYTELPCHLDPCLLQSKESQLLQBENC RKKLEALRADRPAGLLEYLNPNYKDATTMESIVNEYAPLLQQNS KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF VGLSHQYPGPYPLACLLFWPENQELDQDSKLIEKYVSSLNRSFR GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV ISVYSGPLRSGRNIERVSPYLGPSIEQPPGL
6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYPCRGQVVRG PGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH KMVVSIGWNPYYKNTKKSMETHIMHTPKEDFYGEILNVAIVQYL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RPEKNFDSLESLISAIQGDIEEAKKRLELPEHLKIKEDNFFQVS KSKIMNGH
6989	2	1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLV IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE EARLKKSADTLWGIQKELQF
6990	719	258	CHASGMASVVLALRTRTAVTSLLSPTPATALAVRVAGKKSGGSS KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY KTFVHVVPAKPEGTFKLVAML
6991	169	451	RKSSDFHNPGPLSRPVSLRENIHHQVICSTKNKRRNPKKIAYLL SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF CGRHVH
6992	944	510	RQAPGCSSLALRQVRQVVCGLVRAPQVQTRPLSSRFVERRGALY RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPQGY PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLWDMLT
6993	1	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL EAKVRGLERQVEELRWRQRRAAKGARSVEEE
6995	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAVHLAKHRKRIL LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQINAQL EHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTVKTTSRSYQARSLVITAGPWTNQLL RPIGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL
6996	543	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWVFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFLDDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT
6997	370	1104	AMELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRP TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKP YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH VAAECSTWNYFWQQVLDPAWHLLFDGCNLTRESWKALERASFSK LKLQHIQAPLSWELVRPHIYGYAVK
6998	2	616	FVSRALLRVRSRRHPAEERAAPGRPEDAPIECPGATNCPEPLWC SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRLIMQVLKENSLHRALNTLQE ETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDL YEQVVLELIELRELGAARSLLRQTDPMIMLKQTQPERYIHLENL LARSYFDPRDAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMAL LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
7000	2	827	GPGVVFLELMESEGPPESERSEPFSQREEENEEEEAQEPEETGP KNPLLQPALTGDVEGLQKIFEDPENPHHEQAMQLLLEEDIVGRN LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL ETLKALVELDVDIEALNFREERARDVAARYSQTECVEFLDWADA RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN
7001	2056	844	RRCLIIAFLKGCFIFIVPIFIFETEPLSCCPGWSAVAQSRLIAN FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPTI VSPAIVSPTQDSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGQMFRYILNFLRTSKLLIPDDPKDYTLLYEEAKYFQL QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVPPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPIVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLADSSPGLPA RGAEVC
7003	818	61	QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVELLEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRPTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNPCPSLEG
7004	121	2285	FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPPDQECCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GXNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQEFCKAEEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPPDPINPNLHNLNCPVKIKNHNMYVAGCTEVEVKSTEBAFE VFWRGQKKRRIANTHLNRESSRSHSVPNIKLVQAPLDADQDNVL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT LRTCMDVLRENQMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI VCVNPKAEDVEENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQ GKLNEKEKMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEED KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC ERRVAAKQLEMQNKLWVKDEKLKQLKAIVTEPKTEKPERPSRER DREKVTQRSVSPSPVPVSYL
7005	63	876	RNWALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPPKLHL IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS LWRSSG
7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSPFSAGPAT VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS SKLPQNCSELFKTQTPSGDFMHRLPLLGBKQEAKENGTNLTPIG DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS QNLVVLAREDAGAEKIFRSNGVQLLQRLLDMGETDLMLAALRTL VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSIAACHLLQV MFDALKEGVKKGFRGKEGAIIVGENKQVWGLLDVTVMEGMGLSQ PGQFFGDQTCSCRLFGIRFGDIILL
7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLDPGPR SPPPLAGPGQKMVQKKPAELQGFHRSFKGQNPFELAFSLDQPDH GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSPSG RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
7009	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLNLSMPPPKPHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
7010	79	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
7011	3	994	RIQTLPNQNQSQTQPLLKTPPAVLQPIAPQTTFGVQTQPQPQSL LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ RKRSRERSPRRERERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPPQLGNYCNFYVMH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP DPEKDPSVLIKT\AIRCCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSEKPLRPSAARRPEMLSGKKAAAA AAAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL TPEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSEKPLRPSAARRPEMLSGKKAAAA AAAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL TPEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRTGIFPVYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPRRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNISSLN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MELQQLRRMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE ELLQTERDYIRDLEMCIERIMVPMQQAQVFNIDFEGLFGNMQMV IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA LLEIYEKDEKIQKHLQDSLADLKSLVNEWGCTNYINLGSFLIKP VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES ACVKVVAAVSMNDVCMERGHRDLEQFERVHRYISDQLFTNFKER TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCVHGY ABAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ CLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVIKKK DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS TESEHGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPRSGD SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG CARTAQAPEDRSTEPDGSEAEGNQVYPAVTFKARNPNELSVSA NQKLKILEFKDVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT	
7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL GFQRRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITRKETQVILLDTP GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH FKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV KLLK	
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSNGTGMDVSGQETDWRST AFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGM PPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVS TATPQTQLQLQQVAAAAAAATARSSSSSSRRRYSSSSSSSN6KQ FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQQQQHLIKLHHQNQQ QIQQQQQQ-QRIAQLQLQQQQQQQQQQQQQQQQALQAQPPIQQP PMQQPQPPP2SQALPQQLQQNHHTQHHQPPPQPQQPPVAQNQPSQ LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP QVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPF \QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP SKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPVPPTKQQYLCQP LLDAVLANIRSPVPNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA	
7017	1	1785	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPG GETTPSVTDLLNYPLAPEILTGDNQYYCENCASLQNAEKTMQIT EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS SVVVHSGISSESGHTYSYARNITSTDSSYQMYHQSEALALASSQ SHLLGRDSPSAVPEQDLENKEMSKEWPLFNDSRVTFTSFQSVQK ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE LMDAITKDNKLYLQEQELNARARALQAASASCSFRPNGFDDNDP PGSCGPTGGGGGGGFNTVGRLVF
7018	484	1066	SLVFRGNTWSGEAGHHCSALPNLAAVHQLPVGTERIRAPEIIVQ PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQNVFLTGGNTMYP GMKARMEKELLEMRPFRSSPQVQLASNPVLDAWYQARDWALNHL DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA QASSKGSAAGGGGAGEQA
7019	1048	335	APGGFLVTHVFPAFSPPWMLQCCSHEVTAGPPTLCKDMSALVAA RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS SSGALRGVCSCVEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR SQGFPDTYRLPGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK ARESASAKIKEEEAAKD
7020	1	2154	PADSKRKSVLLDKYKNLQVALTSKQQSLETAMSFVARNTFKRVR NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC NIDPSCGFGSNRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI ENVFESAPNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR PGRLLPSFVSSENAFYLSPDIRKQCDWPQGDQPTKNLVKPGHKQ VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTTTTKPVTI INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK PVAAKPAAVRPPPAAAAAKPVATKPEVPRPQAAKPAATKPATTKP MVKMSREVQVFEITENSAKLHWERPEPPGPYFYDLTVTSAHDQS LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSPS TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYYDPNTKSCARFWYGGCGGNENKPGSQKECEKVCA PVLAKPGVISVMGT
7021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS CLGVTDDGMAVATGSWDSFLRIWN
7022	2	856	VYIGSFWSHPLLIPDNRKLPEAEEQDLFRDIQSLPRNAALRKLN DLIKRARLAKVHAYIISSLKKEMPSVPGKDNKKKELVNNLAEIY GRIEREHQISPGDFPNLKRMQDQLQAQDFSKPQPLKSKLLEVVD DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPPGHGYG EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKRKVAE
7023	2	748	AMVEGGVVPYVPQYRDIRRTQNADGPSTYVCLVLLVANYLRILF WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSP TAADSKDEEVKVAPRRSFLDFDPHHFNQWSSPSDYVQCVLAFTG VAGYITYLSIDSALFVSTLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHPTGTKAL
7024	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRGWLLSRQGPASTGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIPDG LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG QDEQPHIPG
7027	43	954	GRRLQQQQRPEDAEDGAEG3GKRGEAGWEGGYPEIVKENKLPEH YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL KNKYFKELEDLEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK SPHLEKPHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD MCAAPGSKTTQLIEMLHADMNVPFPEGPVIANDVDNKRCYLLVH QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRPPPEPEPGTMVEKGSDSSSEKGGVPGTFSTQSLGSRNFIRNS KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR EILLQGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA KLIPNAIQ
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG /PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG R*GKGGPRSPLTKASGTTHIPTPPFFGSIP/RPTRDSGPGTDNS\ AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPLPPL PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG T
7030	2	521	FVCFSAPGSGQGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM EYLVKWKGWSQKYSTWEPEENILQARLLAAFEERERMEMLYGPK KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPVPGRSPQDL ASTSRAREGLRN\RVCPRQRAAPAPAAP\PRRGPSGPGPRPG*G PGLHFPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
7031	960	59	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG /CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC ASQGGPRPTGAGRTPSPLGLPPSRGPPAASARPPCRHPSL
7032	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK SRQIGTSSLPPGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL EPWMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYRQR LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPGPPPLLPV PLA*LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP HHCWVLPPPP*LLLPPR
7033	689	815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMMPSSCPWRTGALGPSPAJGRALGRCTSSVGPGSRWLTRTSSP GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAPPFDELRPLTCDGHDTWGSFSLTLIDALD TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREPYSLKRSRSKPQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPPTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAPPFDELRPLTCDGHDTWGSFSLTLIDALD TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREPYSLKRSRSKPQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPPTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPRRPPRNRRPQ
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPRRPPRNRRPQ
7038	155	891	GAGAASDMSSGLRAADPPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDQTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLANNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADPPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDQTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLANNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KTPPRRPHRCSSGHGSDNSSVLSGELPPAWGKTALFYHSGCSS GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG EPPEIKVYEIDDVERLQRRRGGASKEAMCFNAKLKILEHRQQRI AEVRAKYEWLMKELEATKQYLMLDPNKWLSEFDLEQVWELDSLE YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	1	567	SGRVAMGRRRAPAGGSLGRALMRHQTQRSRSHRHTDSWLHTSEL NDGYDWGRLNLQSVTEQSSLDDFLATAELAGTEFVAEKLNIKPV PAEARTGLLSFEESQRIKKLHEENKQFLCIPRRPNWNQNTTPEE LKQAEKDNFLEWRRQL\VRLEEEQKLILTPFERNLDFWRQLWRV IERSDIVVQIVDA
7042	7	345	PIHMAAAALRADI\ISPLFPHIQGVLLLSASHG\ATSLHTKGAL PLETVTMYTVIPKSKYVLVKPDTQYPYSENLDEFKRLAENSASN DDLLMAEVAISDYGDKLTLELREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD EKGRYKRPHGAPSGGFSAGYFNTVGSKEGWTPSTPVSSRQNRAD KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGQGVGP RVKRRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDYLPDNVTF APKDVTPVDFTPKDNVHGLAYKGLDPHQALPGTSGEHFNLFSGG SERAGDLGEIGLNKGRKLGISGQAPGVGALEEEDDDIYATETLS KYDTVLKDEEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLQV LSESAGKATPDPGTHSKHQLNASKRAELLGETPIQGSATSVLEF LSQXDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSWNMALGGGTATLKASNFKPFAKDPEKQKRYDEFLVHMKQ GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMPGKLTRDTFEW HPDKLLPQ/RLVGLPRVKRDKYSVFNFLTLPBTASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEEHAPELSAN
7044	276	734	EVYLTDEPAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV
7045	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
7046	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
7047	103	486	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVPSYLAGVRSKKALDTAISLGFIISYYER
7048	92	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW
7049	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIANX ASSLWG
7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNY3IRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG
7051	119	816	KKMNLABICDNAKKGREVALLGNYDSSNVYYQGVMQQIQRHCQS VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDPPV SCQDEPPRDPAVWPPPVPAEHRAPPQIRR/RQSRSKTSEERNGR SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDD:ADLBEA KKLLRREAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL TYRNSMYHNKHVFKDKVVLDVGSGTGILSMPAARQGPRR
7054	1	1036	GTSQRSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGPG RRCRWDAMEYDEKLARFRQAHLNPFNKQSGPRQHEQQPGEEVPD VTPEEALPELPPGEPBFRCPERVMDLGLSEDHFSRPVGLFLASD VQQLRQAIBECKQVILELPEQSEKQKDAVVRLIHLRLKLQELKD PNEDEPNIRVLLEHRFYKEKSKSVKQTCDKCNTIIWGLIQTWYT CTGCYYRCHSKCLNLISKPCVSSKVSHQAEYELNICPETGLDSQ DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDLAV IPARVVHNWDFEPRKVSRCSMRYLALWVSRPVLRLRBIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCLPIWLSMNVLLFWKTFLLYNQGP EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG SQKVPSRRTRRLLDKSRTFHITCGATICIPSGVHVAAHLVNALN FSVNYSEDPVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL M
7056	2	527	DSRRV3WRSWLANE/WGKHLCLPIWLSMNVLLFWKTFLLYNQGP EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG SQKVPSRRTRRLLDKSRTFHITCGATICIPSGVHVAAHLVNALN FSVNYSEDPVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL M
7057	1368	431	GIYLIIVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA SGEVPSQASLRGFFTEDEPGCFGEGENLPEALQNIQDEGTGEQL SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRETSQKGQPRAPM AQKLPTCRZCGKTFYRNSQLIFHQRTHTGETYPQCTICKKAFLR SSDFVKHQRTHTGEKPCKCDYCGKGFSDFSCLRHHEKIHTGEKP YKCPICEKSFIQRSNFNRHQRVHTGEKPYKCSHCGKSFSWSSSL DKHQRSHLGKKPFQ*PVTKLSPPISISQPSHKNTQLHQEELCLR GYPC
7058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYNDYLCFRALCCKGPPPAR PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGPSIKAVPFQ NAILNVKELGGADNIRKYWSRYYQQSQGVIFVLDSASSEDDLEA ARN*SCTQLLQHPQLCTLPFLILA
7059	1	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSSI CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP VALQRBPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLP RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRPCCDFRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK TLQHNPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
7060	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNYEYKKLVNPSQ YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKTLHRMAEKVGADITVLRREREVDYDSDMPRKITEVLVRKVPDN QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW*** RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR TAESICESSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCVQEVAGPRE ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAA TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKPKD FYQFTFTPAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTPL MEHH
7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF FTSLWNHPFFTISCITLIGLFPAGIHKRVVAPSIIAARCRTVLA EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS HKGFLLRLDM
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS SRRTGCWTCPPESGHAQARRSRRASASRMGARGAVRSAVAARGC SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS
7065	1	555	ATTCHSARRSGRGAAAEAAASAAGGRQKGPDRKAWEGRRTTPGG RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEABDEIEDI QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL RAGPFDEFQ
7066	356	676	FGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFQHQAPRQLPYKRPDFAQQQAMQ QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ PDAGYYNDLVPPIGMLANNPMNAVTTKFVRTSTNKVKCPVFVVRW TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT HSPFCWAPF
7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD DDDDDDDDDDEDNSLFPTREPRSHFPPPDLFPMCPFGCQCYSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNNKLTKIHPKAPLTTKKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW TLLQSNVPVLQPPLPLEMPPPPPPPPESPPPPPPPPPAPKMPPP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED RVSTAQKRIEEWKQQQLVSGMAERNANPEA
7070	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV LEDEKHHGAQSAALQKVKGQERVRRTSLDLRREIIDVGGIQNLI RLRKKRKQKKRDALAASHEPPPEPEEITGPVDEETPLKAAVEGK MKVIEKPLADGGSADTCDQPRRTALHRASLEGHMEILEKLLDNG ATVDFQ
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7073	50	504	LNHGSPGVSDPPAPAAAPAHTLTSPSGSLSPQPRKPLGRAPAMP LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEPLLGHCIAAGKMNYS VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL AGVFFDRT3LDRKEKLTFTESTHVEI
7075	598	1005	NYINFFFRKEVPPHVQKVEINPVRLSRLQGVERIMKKTEEEESQ VEPRIKRKVQQKRHCSTYQPTPPLSPASKKCLTHLEDLQRNCRQ AITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVSKVP IDII
7076	279	1049	LQSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKGKSH RQDAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV LQQHLETLRQVLTSSPASMPLPEXGETPTVDTIDSYM
7077	3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKANQYLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQPVPHEMPAA RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGEIFFALLRRASPLAHR HLRRQRIDPVLYMTEWPMCIFARTLPWASVLRVWDMPFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDP LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGPSSS
7078	483	767	FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY
7079	2	376	SVVEPKRPKEPSGSDGESDGPIDVGQEQQLSQMARPLSTPSSSQ MQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AEVLQMTVDHLKMLHATGGTGTHALLFQASFIQQIF
7080	200	595	VQLPLEAPCLSLLLSCRDHSGGNRDLSRRHRDCRVYGSPQDGIPY LTHPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS CLFSGDLLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP
7081	213	506	AVTEEEMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVVFRTCEREQN RVVFQMGTS
7082	3	1137	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDIGTGCL SSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSEDPSMLS QAQSATEVEERHVSPSCSTSRERPFQAGBLILAETGEGETKFKK LFRLNNFGLLNSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRP ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH VEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVF YPHLKHGGVCPVYVVNITQVIELLD
7083	115	541	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP SPKAPRARPCRVSTADRSVRKGIMAYSLEDLLLKVRDTLMLADK PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKWQPPSEQG TRHPLSLSHK
7084	3	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK VKNKAPAEVQITAEQLLREAKERELKLLPPPPQQKITDEEELND YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC AELVSFKHPIIVANPRLQMASPEEKCQQVLEPPYDEMFAAHLRCT YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL DLRVFANNADQQLVKKGKSKVGDMLEKAAELLMSCFRVCASDTR AGIEDSKKWGMLFLVNQLFKIYPKINKLHLCKPLIRAIDSSNLK DDYSTAQRVTYKYVVGRKAMFDSDFKQAEEYLSFAFEHCHRSSQ KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG NLLLLHEALAKHEAFFIRCGIFLILEKLKIITYRNLFKKVYLLL KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI SHQHQKLVVSKQNPFPPLSTGC
7086	256	525	ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCP SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCBLDLVY VTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP HRCRVLHNKG
7088	104	759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT MPKAFATAGWLVSLVLLVFLGFMSFMTTTPVIEAMAAANAQLHN KRMENLKEEEDDDSSTASDSDVLIRDNYERAEKRPILSVQRRGS PNPPEITDRVEMGQMASMFPNKVGVNLFYFCIIVYLYGDLAIYA AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK LSAEILRLEKAVQEERTQNQVPKTELARERKDSSLVQLSESKREE TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAPVSVETQ ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC HYTLPPQTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVCFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK LSAEILRLEKAVQEERTQNQVPKTELARERKDSSLVQLSESKREL TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAPVSVETQ ASLLLGLE
7091	186	1076	EQMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGNCKVAIN WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEESQKPRLGEGCEPISKRQMKKLIKQKQWEEQRELR KQRRKEKRKRKKLERQCQMEPNSDGHDRKRVRRDVVHSTLRLII DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSPVIAACQLVLGLLMTSLTESSIQNS ECPQLCVCEIRPWFTPQSTYREA
7094	2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISPFGWWAGEEHPFSFVG DIIAFPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE LLVIRKQQEIDSKDAIILHQPARPNNGVPSLSPFCLKMETYLRM ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR SLECVSHEVDSHYCPSCLENMPSAEAKLKQNRCANCFDCPGCMH TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRRSSRISFAGALPLTRPLLQELLLNNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEAELLLQNLQSKGPRDCVVLMAAAGHPA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ NEESPKQGSGSEGEDGPQVELELVELTVGTLDLCESEVLPKRRR RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL LDEAKAPGQPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANADSRQELQTERISS FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSHDTMTYC LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQALDVTEQ LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISE WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYWWGNRVK TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYCVMRLQT EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSXPLLG LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFLGLNLVL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVABGRTRGR AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPVGCGCFF LGLALRLVYYHWLHPSCCWKPDPDQVD
7099	992	210	LFRLAPGFLRSLARQGYHQIWAFPFLPSGATATWPAASRSRSLA ARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPGAD GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC RQSCQMNNLPHLQVVGLTWGHISWDLLALPPQDIILASDVFFEP EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDM KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSL
7100	205	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL FLFSFPPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWYLIAWEN SSVPVAFSHFRFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7103	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSSES LSDKGSELKKSFDAVVFDVLKVTPEEYAGQITLMDVPVFKAIQP DELSSCGWNKKEKYSSAP
7104	1670	795	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDILYNNAGV MRCPHWTTEDGFEMQFGVNHLGHAWAGAAPWVQAILPRRPPKVL GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASADSRIINLSSLA HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ GSGVTVNALHPGVARTELGRHTGIHGSTFLQHHN\WAHLLAAWS KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAPEAED EEVARRLWAESARLVGLEAPSVREQPLPR
7105	765	143	GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT YFRVGFPGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF GAEFVEVIXDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV TYFEKNFNLRRPNYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF PYIKTRISVIQKEEPVLTPIEVAIEDMKKKTLQLAVAINQEPPD AXMLQMVLQGSVGATVNQGPLEVAQVPLAEIPADPKLYRHHNKL RLCFKEFIMRCGEAVEKNKRLITADQRSYQQELKNYNKLKENL RPMIERRIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS
7107	1145	591	*I*WLQTGKKK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSPTLKMPLFQPVNLNSSTFYIAF FLGRFTGHPGAYLRLINRWLEECHPSGCLIDLCMQMGIIMVLK QTWNNPMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL QPMNAYGLPDEYLEMILQPGFTTIFVAAFPLAPLLALLNNIIEI RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAPVI AITSDPIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS DPENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF WHVLAW
7109	964	102	WDQRKRNSLVPGFAHGPAQSEPWEKKESLGAAQEALSIQLQPKE TQPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM VVIHKEIPTGRKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC SDCGKTFKQSSNLGQHQRIHTGEKPYECNECGKAFRWGAHLVQH QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG KAYGWCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG SPSTKRRGQMLQPIIEGETAHFFEEIKEEEEDGVNLSSELGDML KTAVQVQSSLKNSESDVEENQEKLALDLRRLSSSRAASMPELLEQ LWKARAEKKKLRKTLREPEEAFYQQNGRNAQKEDRVPVLEEYRE YKKIKAKLRLLEVLISKQDSGKSI
7111	2	414	GSGLYRGPTPGGQCIWKPNSMPPDWERNFGFTQFALELNELTAE LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD GAVLW
7112	103	495	PRCFFVADRGRLYGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL ALGLPHLPSPKQRAKPKRVGKEKCRPVLAGGGSGSSAGTPLQHSP LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK SSGPLNLPRR
7114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKYCRKI IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ RIHTSEKPQCSEHGKASDEKPSPTKHVRTHTKENIYECSKCGKS FRGKSHLSVHQRIHTGEKPYECSICGKTFSQKSHLSVHHRTHTG EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK SPLIKHQRIHTGERPYECTDCKKAFSRKSTLIKHQRIHTGEKPY KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSQKSTLI KHQRSHTGDKNL
7115	1	947	NAAHGYNWGLWCNYYIPPQDWLDRGDESAPIRTPAMIGCSPVVD REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN WIKHARH
7116	866	95	RVRMRRNAEVIEHKLSMKSWAKFRPGHPWKGVPNIDPETDPVVT PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELWKVP LPPKNITAPSRPPPGLTGQKPPLSTWDNSPLRIGGGWGNSDARY TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT PHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL
7117	695	1261	LLISTPGGCHPPPSSIEFTYTGAWGKALPAPHMPCAPGALPQGA PVSQAARAIPLLQPSQAAQAEGLSQPARACQALCSLPWPLRNWG SPILRLPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPGGL RVKHRCQPTGHLP
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHPHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTPSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHPHNLVKGLTDLSACKAQLGLGHSYSRAKVKPNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESPSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
7120	1991	64	QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGGGP RABAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGSINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY
7121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ETRQE
7122	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKDQIHIRVSSLLQEAKTQAALVLDCL ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMQSSLKLVDCIIE VHDARIPLSGRNPLFQETLGLKPHLLVLNKNDLADLTEQQKIMQ HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYIHRENL EYCIMVIGVPNVGKSSLINSLRRQHLRKGKATRVGGEPGITRAV MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL VGEETMADYLLYTLNKHQRFGYVQHYGLGSACDNVERVLKSVAV KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM LDLDVLRGHPRV
7124	2	382	LPLTLLLAAPFAHLLPPGHDQSPCWHPGPALSPGTLGPLSWAM ANSGLQLLGYPLALGGWVGIIASTALPQWKQSSYAGDASIQLRS KVPVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSRIRRRKLCGSSESRGVNESHKSE FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLLALCTPLVSEKH AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAAFNE ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGPVSVHNPH ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRGQERGT SHSQAREPQRPGRWLLGSLQSSPGTLGQAGTASRRRQCMVQRNV QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIP AKQKQI*S*NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV *FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L CQSSLRDQTIVTWRM*RNYSMPRINMISSL*DGSIHIPLKLHFY PALIPTLTVPINSCCQRPLPLPAHQSIKTLASGSPMLACLRFL LVKKRAFIHTPRSPQCSV*CKHVLVKDNKNNCVQSEV
7128	2	5228	GRVDLWTILLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSP SSAEKVKANKDVASPLKELGLRISKPLGLDEEQSVQLLQCYLQE DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHL LTYPQDERHPYRVEYADCVDKLEKELVSKYRQQPEELYKTEAPT WETHGNLMTERQVSRWFVQCLREQSMLLEIIPLYYAYPEMAPGD LLVLTKMFKEQGFGSRQTNRHLVDETNDPFVDRIGYFSALILVE GMDIESLHKCALDDRRELHQFAQDQLICQDMDCLMLTFGDIPHH APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLLQ SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL RALVSGKSTAKKVYSFLDKNSFYNELYKHKPHDVISHEDGTLWR RQTPKLLYPLGGQTNLRIPQQTVGQVMLDDRAYLVRWEYDYSSW TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA KVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSE OPQGEYGVTIAFLRLITTLVKGGLGSTQSQGLVPCVMFVLKEML

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PSYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPS LQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEG QGQGQLLIKTVKLAPSVTNNVIRLKPPSNVVSPLEQALSQHGAH GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLG NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQM LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRKML QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRYLRD PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR
7129	1	1054	FRRFRWRRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSRIL MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFA TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKGL
7130	2	780	HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGRKG ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHRSS RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLPLN AQIATQNYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLTP YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLEVV KLLQDYQDSYTLSETQAEAAAERALSKENLESMV
7132	1420	1087	IDMLLLSGALVSGPVTLITTAVSADLGTHKSLKGNAHALSTVTA IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI RLIHKELSCPGSATGDQVPPKEQ
7133	2	3648	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLPFTLYPSLEKF EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRSRL RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS RVAQDCRGTSWPKTVYPTFQFYRPPPATTPRLQLVQLDEAGQPS SGALTHILVPVSRDGTFDAGSPGFQLRYMVGPGFLKPGERRCFA RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQASHE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEVVATEYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRLHLTLAN VGHIPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLLTTGSSRR KHVVQAQKLADVDSELAAMLLTHARQGKGPQDVSRESDATRRRK LERMRSVRLQEAGGDLGRRGTSVLAQQSVRTQHLRDLQVIAAYR ERTKAESIASLLSLAITTEHTLHATLGVABFPSEPVLKNPHNTQH TVTVEIDNPELSVIVDSQEWRDPKGAAGLHTPVEEDMFHLRGSL APQLYLRPHETAHVPPFKPQSFSAGQLAMVQASPGLSNEKGMDAV SPWKSSAVPTKHAKVLFRASGGKPIAVLCLTVELQPHVVDQVFR FYHPELSFLKKAIRLPPWHTFPGAPVGMLGEDPPVHVRCSDPNV ICETQNVGPGEPRDIPLKVASGPSPEIKDFFVIIYSDRWLATPT QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAPTSH PQELKTDPKGVPVLPPRGVQDLHVGVRPLRAGSRPVHLNLVDVD CHQLVASWLVCLCCRQPLISKAFEIMLAAGEGKGVNKRITYTNP YPSRRTPHLHSDHPELLRPREDSFQVGGGETYTIGLQFAPSQRV GEEEILIYINDHEDKNEEAFCVKVIYQ
7134	2115	1111	GGEGFSYPPHVGLSLGTPLDPHVLLEVHYDNPTYEEGLIYNSG LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTL ECLEEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGKEMKL LAYDDDFDFNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT WGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEI YRPVTTWPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVL SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLSCTLSTKSL
7135	2	2072	FVPRVTPRSLSLQGPKGESVGSITQPLPSSYLIFRAASESDGRC WLDALELALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAPSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGPCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEQGSSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRAEREQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSANLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK
7136	2	418	DFVPSFRRFSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGGIRISKPPSPKPMPV IRVVET
7137	2	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7138	2	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7139	1	357	SLRNSARGLKMAASAARGAAALRRSINQPVAPVRRIPWTAASSQ LKEHPAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF
7140	1401	1957	RASSLQVLKAWGGLIPSSPQQQHTGQYALEELFDLKVYDCPCSF NMNVSLEKQLRPSQPWPRGKCRKTPGWEEARPKAQDLRGDLGKT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADFMTNQCG
7141	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP
7142	658	839	LIFLMLHMELKMLSSVTLHIRAPLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEPIEEAKRKDGVVLVHCNA
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/34263

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00
US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 536/23.1; 435/320.1, 455, 468, 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
MEDLINE, EAST

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82	1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.	1-11, 13-16, and 19-26

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
	07 JUN 2001
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Michael Woodward Telephone No. (703)308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This includes 4 invention Groups and 3572 sequence species

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid.
Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides.
Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies.
Group III, claims 17-18, drawn to methods of indentifying a binding partner to a polypeptides.
Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups.Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as representde by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☑ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.